

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 31.2821 Seconds
(without alignments)
170.386 Million cell updates/sec

Title: US-09-780-438C-1
Perfect score: 211
Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

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9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

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18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

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20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	80	16	AA1980
2	211	100.0	80	20	AA1981
3	211	100.0	80	22	AA1982
4	211	100.0	523	22	AA1983
5	211	100.0	524	16	AA1984
6	211	100.0	524	20	AA1985
7	211	100.0	524	21	AA1986
8	211	100.0	527	22	AA1987
9	211	100.0	592	22	AA1988
10	127	60.2	25	22	AA1989

11	111	52.6	22	16	AA1980	Saposin-C neurotro
12	111	52.6	22	18	AA1981	Prosaposin-derived
13	111	52.6	22	19	AA1982	Prosaposin recepto
14	111	52.6	22	20	AA1983	Prosaposin recepto
15	111	52.6	22	22	AA1984	Peptide #5. Homo
16	106	50.2	22	18	AA1985	Mutant human prosa
17	106	50.2	22	19	AA1986	Prosaposin derivat
18	103	48.8	21	21	AA1987	Human saposin C 22
19	99	46.9	25	22	AA1988	Bovine saposin C.
20	96	45.5	22	18	AA1989	Bovine prosaposin-
21	96	45.5	22	19	AA1990	Prosaposin recepto
22	96	45.5	22	20	AA1991	Prosaposin recepto
23	83	39.3	18	16	AA1992	Saposin-C derived
24	83	39.3	18	18	AA1993	Saposin C 12 to 29
25	83	39.3	18	19	AA1994	Prosaposin recepto
26	83	39.3	18	20	AA1995	Prosaposin recepto
27	83	39.3	18	21	AA1996	Human saposin C 18
28	80	37.9	25	22	AA1997	Guinea pig saposin
29	78	37.0	554	23	AA1998	Mouse ischaemic co
30	75	35.5	15	19	AA1999	Human saposin C de
31	75	35.5	15	20	AA2000	Human saposin C fr
32	75	35.5	15	21	AA2001	Human saposin C pe
33	75	35.5	22	18	AA2002	Guinea pig prosapo
34	75	35.5	22	19	AA2003	Prosaposin recepto
35	75	35.5	22	20	AA2004	Prosaposin recepto
36	73	34.6	514	23	AA2005	Theobroma cacao as
37	73	34.6	514	23	AA2006	Theobroma cacao as
38	73	34.6	953	22	AA2007	Drosophila melanog
39	70	33.2	149	21	AA2008	Arabidopsis thalia
40	70	33.2	205	21	AA2009	Arabidopsis thalia
41	70	33.2	298	21	AA2010	Arabidopsis thalia
42	70	33.2	506	21	AA2011	Arabidopsis thalia
43	70	33.2	522	21	AA2012	Arabidopsis thalia
44	67	31.8	80	22	AA2013	Human eSAP-C prote
45	67	31.8	345	22	AA2014	Human gene 1 encod

ALIGNMENTS

RESULT 1

AA1980

ID AAR70784 standard; Protein; 80 AA.

XX AAR70784;

AC AAR70784;

XX AAR70784;

DT 30-AUG-1995 (first entry)

XX Saposin-C.

XX Saposin-C; neuron; myelination; nervous system; neuroblastoma;

KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;

KW adrenal leukodystrophy.

XX Homo sapiens.

OS Homo sapiens.

XX WO9503821-A.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US08453.

XX 30-JUL-1993; 93US-0100247.

XX 21-APR-1994; 94US-0232513.

XX (OBRI/) OBRIEN-J-S.

XX Kishimoto Y, Obrien JS;

XX WPI; 1995-082029/11.

XX Stimulating neural cell out-growth and myelination - with

PT pro:saposin, saposin C or new neurotrophic peptide(s) from

PT cytokine(s), for treating nervous system diseases

XX Disclosure; Page 32; 50pp; English.

XX
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.
CC A consensus sequence was determined by comparing the peptide with
CC hematopoietic and neuropoietic cytokines, and neurotrophic peptides
CC (AAR70774-82) were identified in the AB loop of human ciliary
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,
CC erythropoietin and leukocyte inhibitory factor, and in helix C of
CC human interleukin-1-beta and oncostatin-M. Prosapoinin (AAR70783)
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX Sequence 80 AA;

Query Match 100.0%; Score 211; DB 16; Length 80;
Best Local Similarity 100.0%; Pred. No. 9.9e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
|||||
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 2

AAW85653

ID AAW85653 standard; Peptide; 80 AA.

XX AAW85653;

DT 19-JUL-1999 (first entry)

DE Human saposin C.

XX
KW Prosapoinin; saposin; prosaptides; prosapoinin receptor agonists;
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;
KW inflammation; rheumatoid arthritis; Crohn's disease;
KW irritable bowel syndrome; asthma; cardiac infarction;
KW congestive heart failure; multiple sclerosis;
KW acute disseminated inflammatory leukoencephalitis;
KW progressive multifocal leukoencephalitis; Alzheimer's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis;
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;
KW inflammatory neurodegenerative disease; toxin-induced liver disease.

XX Homo sapiens.

XX WO9912559-A1.

XX 18-MAR-1999.

XX 09-SEP-1998; 98WO-US19216.

XX 04-JUN-1998; 98US-0088129.

XX 09-SEP-1997; 97US-0058352.

XX (REGC) UNIV CALIFORNIA.

XX O'brien JS;

XX WPI; 1999-229139/19.

XX Use of prosapoinin receptor agonist

XX Claim 7; Figure 2; 90pp; English.

XX Prosapoinin is a 70kDa glycoprotein which is proteolytically processed
CC to generate saposins A, B, C and D, all of which are similar to each
CC other and have a similar placement of six cysteines, a glycosylation

CC site and conserved proline residues. Prosapoinin, saposin C and
CC prosapoinin derived peptides (prosaptides), have therapeutic
CC applications in promoting recovery after toxic, traumatic, myocardial
CC ischaemic, degenerative and inherited lesions to the peripheral and
CC central nervous system. Prosapoinin receptor agonists (PRAS)
CC inhibit proinflammatory cytokine-induced apoptosis by activation of
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family
CC members which inhibit caspases, thereby inhibiting apoptosis. An
CC additional mechanism whereby PRAS inhibit apoptosis is by blocking
CC activation of JNK, a proapoptotic signaling component. Within
CC several minutes after binding to the receptor, PRAS block JNK
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced
CC apoptosis. The method can be used for inhibiting apoptosis which is
CC caspase-mediated or induced by a proinflammatory cytokine, for
CC example TNF alpha or interferon-gamma. It can be used for inhibiting
CC apoptosis associated with a disorder such as e.g. rheumatoid
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac
CC infarction, congestive heart failure, multiple sclerosis, acute
CC disseminated inflammatory leukoencephalitis, progressive multifocal
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced
CC liver disease. Saposin C acts as a prosapoinin receptor agonist.

XX Sequence 80 AA;

Query Match 100.0%; Score 211; DB 20; Length 80;
Best Local Similarity 100.0%; Pred. No. 9.9e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
|||||
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 3

AAU05697

ID AAU05697 standard; Protein; 80 AA.

XX AAU05697;

XX 24-OCT-2001 (first entry)

XX Human Saponin C, SapC.

XX Human; glucocerebrosidase; GCB; lysosomal storage disease;
KW Gaucher's disease; Fabry's disease; Farber's disease;
KW G_m_1 gangliosidosis; Tay-Sach's disease; Niemann-Pick disease;
KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;
KW Scheie syndrome; Saponin C; SapC.

OS Homo sapiens.

XX WO200149830-A2.

XX 12-JUL-2001.

XX 29-DEC-2000; 2000WO-DK00743.

XX 30-DEC-1999; 99DK-0001891.

XX 02-JUN-2000; 2000DK-0000865.

XX 02-JUN-2000; 2000DK-0000866.

XX 30-JUN-2000; 2000DK-0001027.

XX (MAXY-) MAXYGEN APS.

XX Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;

DR WPI; 2001-465259/50.

XX Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -

XX Example 5; Page 96; 97pp; English.

PS The sequence represents human Saponin C (SapC), an essential

XX co-factor for the lysosomal enzyme glucocerebrosidase,

CC GCB. GCB is the enzyme involved in Gaucher's disease, a lysosomal

CC storage disease. The invention relates to introducing new glycosylation

CC sites into lysosomal enzymes/activators like GCB to improve their

CC bioactivity. The novel polypeptides are used for the prevention and

CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,

CC G_m1 gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler

CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie

CC syndromes.

XX

SQ Sequence 80 AA;

Query Match 100.0%; Score 211; DB 22; Length 80;

Best Local Similarity 100.0%; Pred. No. 9.9e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 4

AAB31916

ID AAB31916 standard; Protein; 523 AA.

XX

AC AAB31916;

XX

DT 15-MAY-2001 (first entry)

XX

DE Amino acid sequence of a human protein.

XX

KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;

KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;

KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;

KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;

KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200105422-A2.

XX

PD 25-JAN-2001.

XX

PF 17-JUL-2000; 2000WO-FR02057.

XX

PR 15-JUL-1999; 99FR-0009372.

XX

PA (INMR) BIOMERIEUX STELHYS.

XX

PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX

DR WPI; 2001-159475/16.

XX

PT Detecting, preventing and treating degenerative, neurological and

PT autoimmune diseases, particularly multiple sclerosis, using specified

PT polypeptides or related nucleic acid or ligand -

XX

PS Claim 1; Page 174-175; 209pp; French.

XX

CC The present sequence represents a human protein, which is used in the

CC method of the invention. The specification describes a method which uses

CC at least one polypeptide or polynucleotide sequence belonging to the

CC perlecan, precursor of the retinol-binding plasma protein, precursor of

CC the ganglioside GM2 activator, calgranulin B or saposin B protein

CC families. The method is used for detecting, preventing or treating a

CC degenerative, neurological and/or auto-immune disease. The

CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms

CC and phases). They may also be useful in cases of e.g. Alzheimer's and

CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid

CC polyarthritis and lupus erythematosus, including use as vaccines and

CC in gene therapy (expression of sense or antisense sequences). They can

CC also be used to assess efficacy of potential therapeutic agents,

CC particularly compounds that reduce or inhibit toxicity towards glial

CC cells.

XX

SQ Sequence 523 AA;

Query Match 100.0%; Score 211; DB 22; Length 523;

Best Local Similarity 100.0%; Pred. No. 8.7e-19;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 349

RESULT 5

AAR70783

ID AAR70783 standard; Protein; 524 AA.

XX

AC AAR70783;

XX

DT 30-AUG-1995 (first entry)

XX

DE Prosaposin.

XX

KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;

KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;

KW adrenal leukodystrophy; prosaposin.

XX

OS Homo sapiens.

XX

PN WO9503821-A.

XX

PD 09-FEB-1995.

XX

PF 28-JUL-1994; 94WO-US08453.

XX

PR 30-JUL-1993; 93US-0100247.

PR 21-APR-1994; 94US-0232513.

XX

PA (OBRI/) OBRIEN J S.

XX

PI Kishimoto Y, Obrien JS;

XX

DR WPI; 1995-082029/11.

DR N-PSDB; AAQ85355.

XX

PT Stimulating neural cell out-growth and myelination - with

PT pro:saposin, saposin C or new neurotrophic peptide(s) from

PT cytokine(s), for treating nervous system diseases

XX

PS Disclosure; Page 30-32; 50pp; English.

XX

CC The peptide given in AAR70773, corresponding to amino acids 8-29 of

CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.

CC A consensus sequence was determined by comparing the peptide with

CC hematopoietic and neuroepithelial cytokines, and neurotrophic peptides

CC (AAR70774-82) were identified in the AB loop of human ciliary

CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,

CC erythropoietin and leukocyte inhibitory factor, and in helix C of

CC human interleukin-1-beta and oncostatin-M. Prosaposin (AAR70783)

CC and saposin-C also promoted nerve cell myelination ex vivo.

XX

SQ Sequence 524 AA;

Query Match 100.0%; Score 211; DB 16; Length 524;

Best Local Similarity 100.0%; Pred. No. 8.8e-19; Mismatches 0; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
|||||
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 6
AAW85652
ID AAW85652 standard; Protein; 524 AA.
XX AAW85652;
AC AAW85652;
XX 19-JUL-1999 (first entry)
XX Human prosaposin N-terminal peptide.
DE Prosaposin; saposin; prosaptides; prosaposin receptor agonists;
XX PRA; peripheral nervous system; central nervous system; PNS; CNS;
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;
KW inflammation; rheumatoid arthritis; Crohn's disease;
KW irritable bowel syndrome; asthma; cardiac infarction;
KW congestive heart failure; multiple sclerosis;
KW acute disseminated inflammatory leukoencephalitis;
KW progressive multifocal leukoencephalitis; Alzheimer's disease;
KW Parkinson's disease; amyotrophic lateral sclerosis;
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;
KW inflammatory neurodegenerative disease; toxin-induced liver disease.
XX Homo sapiens.
OS Homo sapiens.
XX WO9912559-A1.
PN 18-MAR-1999.
XX 09-SEP-1998; 98WO-US19216.
XX 04-JUN-1998; 98US-0088129.
PR 09-SEP-1997; 97US-0058352.
XX (REGC) UNIV CALIFORNIA.
XX O'brien JS;
PI WPI; 1999-229139/19.
XX N-PSDB; AAX08488.
DR Use of prosaposin receptor agonist
XX Claim 7; Figure 2; 90pp; English.
PS Prosaposin is a 70kDa glycoprotein which is proteolytically processed
XX to generate saposins A, B, C and D, all of which are similar to each
CC other and have a similar placement of six cysteines, a glycosylation
CC site and conserved proline residues. Prosaposin, saposin C and
CC prosaposin derived peptides (prosaptides), have therapeutic
CC applications in promoting recovery after toxic, traumatic, myocardial
CC ischaemic, degenerative and inherited lesions to the peripheral and
CC central nervous system. Prosaposin receptor agonists (PRAS)
CC inhibit proinflammatory cytokine-induced apoptosis by activation of
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family
CC members which inhibit caspases, thereby inhibiting apoptosis. An
CC additional mechanism whereby PRAS inhibit apoptosis is by blocking
CC activation of JNK, a proapoptotic signaling component. Within
CC several minutes after binding to the receptor, PRAS block JNK
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The
CC activation of JNK by TNF alpha is another well known mechanism for
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced
CC apoptosis. The method can be used for inhibiting apoptosis which is

CC caspase-mediated or induced by a proinflammatory cytokine, for
CC example TNF alpha or interferon-gamma. It can be used for inhibiting
CC apoptosis associated with a disorder such as e.g. rheumatoid
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac
CC infarction, congestive heart failure, multiple sclerosis, acute
CC disseminated inflammatory leukoencephalitis, progressive multifocal
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced
CC liver disease. This 524 N-terminal peptide of prosaposin also acts
CC as a prosaposin receptor agonist.
XX
SQ Sequence 524 AA;
Query Match 100.0%; Score 211; DB 20; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
|||||
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 7
AAW58716
ID AAY58716 standard; Protein; 524 AA.
XX AAY58716;
AC AAY58716;
XX 25-APR-2000 (first entry)
XX Human prosaposin.
DE Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;
KW antitumour; antiproliferative; antimigratory; Kaposi's sarcoma;
KW tumour; human; therapy.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Protein 195..275
FT /note= "mature saposin B"
FT Peptide 195..205
FT /note= "specifically claimed antiangiogenic peptide
FT of Claim 23"
FT Peptide 196..200
FT /note= "specifically claimed antiangiogenic peptide
FT of Claim 4"
XX WO200002902-A1.
PN 20-JAN-2000.
XX 12-JUL-1999; 99WO-US15772.
XX 13-JUL-1998; 98US-0092647.
XX (GILL/) GILL P S.
PI Gill PS;
XX WPI; 2000-171128/15.
XX Saposin B derived peptides, useful as inhibitors of angiogenesis and
PT tumor growth -
XX Disclosure; Page 18; 78pp; English.
XX The present sequence is that of human prosaposin, a precursor of
CC saposin B. The invention is based on the discovery that saposin B,
CC previously known to be involved in the hydrolysis of sphingolipids,

CC has potent antiangiogenic and antitumour activity, and also has
CC antiproliferative and antimigratory activity against endothelial
CC cells. This activity is conserved in cryptic polypeptides as small
CC as 5 amino acids (see AAY58684-715), which can be synthetically
CC prepared and used in vitro or in vivo for the treatment of
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma
CC (claimed). The polypeptides can also be used in conjunction with
CC cytotoxic moieties to selectively kill certain cell types, e.g. for
CC treatment of cancer, angiofibroma, neovascular glaucoma,
CC arteriovenous malformation, nonunion fracture, arthritis and other
CC connective tissue disorders, Osler-Weber syndrome, atherosclerotic
CC plaque, psoriasis, corneal graft neovascularization, pyogenic
CC granuloma, retrolental fibroplasia, diabetic retinopathy,
CC scleroderma, haemangioma, trachoma, vascular adhesions and
CC hypertrophic scars.

XX
SQ Sequence 524 AA;

Query Match 100.0%; Score 211; DB 21; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
|||||
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 350

RESULT 8

AAB31915
ID AAB31915 standard; Protein; 527 AA.

XX
AC AAB31915;

XX
DT 15-MAY-2001 (first entry)

XX
DE Amino acid sequence of a human protein.

XX
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.

XX
OS Homo sapiens.

XX
PN WO200105422-A2.

XX
PD 25-JAN-2001.

XX
PF 17-JUL-2000; 2000WO-FR02057.

XX
PR 15-JUL-1999; 99FR-0009372.

XX
PA (INMR) BIOMERIEUX STELHYS.

XX
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;

XX
DR WPI; 2001-159475/16.

XX
PT Detecting, preventing and treating degenerative, neurological and
PT autoimmune diseases, particularly multiple sclerosis, using specified
PT polypeptides or related nucleic acid or ligand -

XX
PS Claim 1; Page 172-173; 209pp; French.

XX
CC The present sequence represents a human protein, which is used in the
CC method of the invention. The specification describes a method which uses
CC at least one polypeptide or polynucleotide sequence belonging to the
CC perlecan, precursor of the retinol-binding plasma protein, precursor of
CC the ganglioside GM2 activator, calgranulin B or saposin B protein
CC families. The method is used for detecting, preventing or treating a
CC degenerative, neurological and/or auto-immune disease. The
CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms
CC and phases). They may also be useful in cases of e.g. Alzheimer's and
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid
CC polyarthritis and lupus erythematosus, including use as vaccines and
CC in gene therapy (expression of sense or antisense sequences). They can
CC also be used to assess efficacy of potential therapeutic agents,
CC particularly compounds that reduce or inhibit toxicity towards glial
CC cells.

XX
SQ Sequence 527 AA;

Query Match 100.0%; Score 211; DB 22; Length 527;
Best Local Similarity 100.0%; Pred. No. 8.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
|||||
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 353

RESULT 9

AAB31915
ID AAB31915 standard; Protein; 592 AA.

XX
AC AAB31915;

XX
DT 24-OCT-2001 (first entry)

XX
DE Human glucocerebrosidase, GCB-Saponin C, SapC, fusion protein.

XX
KW Human; glucocerebrosidase; GCB; lysosomal storage disease;
KW Gaucher's disease; Fabry's disease; Farber's disease;
KW G_m1 gangliosidosis; Tay-Sachs's disease; Niemann-Pick disease;
KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;
KW Schele syndrome; fuslon protein; Saponin C; SapC.

XX
OS Homo sapiens.

OS
Synthetic.

XX
FH Key Location/Qualifiers
FT Protein 1..80
FT Peptide /label= SapC
FT /label= Linker_peptide
FT Protein 96..592
FT /label= GCB
FT Modified-site 114
FT /note= "N-glycosylated"
FT Modified-site 154
FT /note= "N-glycosylated"
FT Modified-site 241
FT /note= "N-glycosylated"
FT Modified-site 365
FT /note= "N-glycosylated"

XX
PN WO200149830-A2.

XX
XX 12-JUL-2001.

XX
XX 29-DEC-2000; 2000WO-DK00743.

XX
PR 30-DEC-1999; 99DK-0001891.

PR 02-JUN-2000; 2000DK-0000865.

PR 02-JUN-2000; 2000DK-0000866.

PR 30-JUN-2000; 2000DK-0001027.

XX
PA (MAXY-) MAXYGEN APS.

XX
PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;

XX
DR WPI; 2001-465259/50.

XX
PT Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -
PS Example 5; Page 96-97; 97pp; English.
XX
CC The sequence is a fusion protein of human lysosomal enzyme
CC glucocerebrosidase, GCB and its co-factor, Saponin C, SapC.
CC GCB is the enzyme involved in Gaucher's disease, a lysosomal
CC storage disease. The invention relates to introducing new glycosylation
CC sites into lysosomal enzymes/activators like GCB to improve their
CC bioactivity. The novel polypeptides are used for the prevention and
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,
CC G_m_1 gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie
CC syndromes.
XX
SQ Sequence 592 AA;

Query Match 100.0%; Score 211; DB 22; Length 592;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADKMSKLP 40
DB 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADKMSKLP 40

RESULT 10
AAB67289
ID AAB67289 standard; Peptide; 25 AA.
XX
AC AAB67289;
XX
DT 20-APR-2001 (first entry)
XX
DE Human saposin C.
XX
KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.
XX
OS Homo sapiens.
XX
PN EP1072609-A2.
XX
PD 31-JAN-2001.
XX
PF 30-JUN-2000; 2000EP-0305504.
XX
PR 30-JUN-1999; 99JP-0185155.
XX
PA (SAKA/) SAKANAKA M.
PA (TANA/) TANAKA J.
PA (SATO/) SATO K.
XX
PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;
XX WPI; 2001-204263/21.
DR
XX
PT Use of prosaposin-related peptides or derivatives as cytoprotective
PT agents, for suppressing apoptosis or apoptosis-like cell death -
XX
PS Disclosure; Page 12; 41pp; English.
XX
CC The present invention relates to use of a prosaposin-related peptide
CC or derivative, in the production of a medicament for use in
CC preventing or delaying cell death, or in promoting the expression
CC of cell death supporting gene product Bcl-XL. The invention is
CC useful for preventing the death of cells e.g. brain cells,
CC neurons and cardiac muscle cells, in vitro or ex vivo.
XX
SQ Sequence 25 AA;

Query Match 60.2%; Score 127; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEILDAD 32
DB 1 CEFLVKEVTKLIDNNKTEKEILDAD 25

RESULT 11
AAR70773
ID AAR70773 standard; peptide; 22 AA.
XX
AC AAR70773;
XX
DT 30-AUG-1995 (first entry)
XX
DE Saposin-C neurotrophic peptide.
XX
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;
KW adrenal leukodystrophy.
XX
OS Homo sapiens.
XX
PN WO9503821-A.
XX
PD 09-FEB-1995.
XX
PF 28-JUL-1994; 94WO-US08453.
XX
PR 30-JUL-1993; 93US-0100247.
PR 21-APR-1994; 94US-0232513.
XX
PA (OBRI/) OBRIEN J S.
XX
PI Kishimoto Y, Obrien JS;
XX WPI; 1995-082029/11.
XX
PT Stimulating neural cell out-growth and myelination - with
PT pro:saposin, saposin C or new neurotrophic peptide(s) from
PT cytokine(s), for treating nervous system diseases
XX
PS Disclosure; Page 30; 50pp; English.
XX
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.
CC A consensus sequence was determined by comparing the peptide with
CC hematopoietic and neuroepithelial cytokines, and neurotrophic peptides
CC (AAR70774-82) were identified in the AB loop of human ciliary
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,
CC erythropoietin and leukocyte inhibitory factor, and in helix C of
CC human interleukin-1-beta and oncostatin-M. Prosaposin (AAR70783)
CC and saposin-C also promoted nerve cell myelination ex vivo.
XX
SQ Sequence 22 AA;

Query Match 52.6%; Score 111; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
DB 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 12
AAW30013
ID AAW30013 standard; peptide; 22 AA.
XX
AC AAW30013;
XX
DT 14-APR-1998 (first entry)
XX
DE Prosaposin-derived peptide 22-mer.

XX Human; prosaposin; neural disorder; demyelination disorder;
 KW neural cell death; inhibition; myelination; neurite outgrowth;
 KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;
 KW polyneuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus.
 XX Homo sapiens.
 OS WO9732895-A1.
 PN 12-SEP-1997.
 XX 05-MAR-1997; 97WO-US04143.
 XX 05-MAR-1996; 96US-0611307.
 PR (REGC) UNIV CALIFORNIA.
 PA O'Brien JS;
 PI WPI; 1997-470538/43.
 XX Prosaposin-derived peptide - useful for therapy of neural or
 DR demyelination disorders in neural tissue
 PT Claim 9; Page 52; 69pp; English.
 XX The present sequence represents a prosaposin-derived peptide. A method
 CC has been developed of alleviating or preventing neuropathic pain in a
 CC subject, comprising administering an effective amount of an active
 CC fragment of prosaposin to the subject. The prosaposin-derived peptide
 CC is useful for therapy of neural or demyelination disorders in neural
 CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural
 CC cell death, promote myelination or inhibit demyelination. The method
 CC is used to alleviate neuropathic pain resulting from a peripheral nerve
 CC disorder, such as neuroma, nerve compression, crush or stretch and
 CC incomplete nerve transection, mononeuropathy or polyneuropathy.
 CC Alternatively the neuropathic pain results from a disorder of the
 CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.
 XX
 SQ Sequence 22 AA;
 Query Match 52.6%; Score 111; DB 18; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CEFLVKEVTKLIDNNKTEKIL 29
 Db 1 CEFLVKEVTKLIDNNKTEKIL 22
 RESULT 13
 AAW66127
 ID AAW66127 standard; peptide; 22 AA.
 XX AAW66127;
 AC 17-NOV-1998 (first entry)
 DT Prosaposin receptor agonist #1.
 XX prosaposin; receptor agonist; neuropathic pain; neurite outgrowth;
 KW neural cell death; nerve disorder; side effect.
 XX Synthetic.
 OS Homo sapiens.
 OS WO9839357-A1.
 PN 11-SEP-1998.
 XX 11-SEP-1997; 97WO-US16062.
 PF
 XX

PR 05-MAR-1997; 97WO-US04143.
 XX (REGC) UNIV CALIFORNIA.
 PA O'Brien JS;
 PI WPI; 1998-495790/42.
 DR N-PSDB; AAV07664.
 XX Use of prosaposin receptor agonists - for alleviating neuropathic
 PT pain, inhibiting sensory or motor neuropathy, or inhibiting neural
 PT cell death
 XX Claim 3; Page 2; 67pp; English.
 PS The invention relates to prosaposin receptor agonists. Also claimed
 XX are: (1) methods for alleviating neuropathic pain or inhibiting the
 CC onset of neuropathic pain, comprising administering a prosaposin receptor
 CC agonist; (2) inhibiting sensory or motor neuropathy, comprising
 CC contacting neuronal cells with a composition comprising a prosaposin
 CC receptor agonist; (3) methods for stimulating myelination, or inhibiting
 CC inhibiting neural cell death, promoting myelination, or inhibiting
 CC demyelination comprising contacting neuronal cells with a composition
 CC comprising a prosaposin receptor agonist which has 14-50 amino acids and
 CC comprises the sequence of a prosaposin derived protein. The processes
 CC may be used for treatment of neuropathic pain resulting from peripheral
 CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve
 CC stretch, incomplete nerve transection, mononeuropathy or polyneuropathy)
 CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the
 CC thalamus or the cortex. The receptor agonists do not cause undesirable
 CC side effects. The present sequence represents a specifically claimed
 CC prosaposin receptor agonist.
 XX
 SQ Sequence 22 AA;
 Query Match 52.6%; Score 111; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CEFLVKEVTKLIDNNKTEKIL 29
 Db 1 CEFLVKEVTKLIDNNKTEKIL 22
 RESULT 14
 AAW85656
 ID AAW85656 standard; Peptide; 22 AA.
 XX AAW85656;
 AC 19-JUL-1999 (first entry)
 DT Prosaposin receptor agonist.
 XX Prosaposin; saposin; prosaptides; prosaposin receptor agonists;
 KW PRA; peripheral nervous system; central nervous system; PNS; CNS;
 KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;
 KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;
 KW inflammation; rheumatoid arthritis; Crohn's disease;
 KW irritable bowel syndrome; asthma; cardiac infarction;
 KW congestive heart failure; multiple sclerosis;
 KW acute disseminated inflammatory leukoencephalitis;
 KW progressive multifocal leukoencephalitis; Alzheimer's disease;
 KW Parkinson's disease; amyotrophic lateral sclerosis;
 KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;
 KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;
 KW inflammatory neurodegenerative disease; toxin-induced liver disease.
 XX Homo sapiens.
 OS WO9912559-A1.
 PN 18-MAR-1999.
 XX PD

XX PF 09-SEP-1998; 98WO-US19216.
XX PR 04-JUN-1998; 98US-0088129.
XX PR 09-SEP-1997; 97US-0058352.
XX PA (REGC) UNIV CALIFORNIA.
XX PI O'brien JS;
XX DR WPI; 1999-229139/19.
XX PT Use of prosaposin receptor agonist
XX PS Claim 7; Page 66; 90pp; English.
XX CC

Prosaposin is a 70kDa glycoprotein which is proteolytically processed to generate saposins A, B, C and D, all of which are similar to each other and have a similar placement of six cysteines, a glycosylation site and conserved proline residues. Prosaposin, saposin C and prosaposin derived peptides (prosaptides), have therapeutic applications in promoting recovery after toxic, traumatic, myocardial ischaemic, degenerative and inherited lesions to the peripheral and central nervous system. Prosaposin receptor agonists (PRAs) inhibit proinflammatory cytokine-induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2 family members, such as BAD-Bcl-2, releasing Bcl-2 and its family members which inhibit caspases, thereby inhibiting apoptosis. An additional mechanism whereby PRAs inhibit apoptosis is by blocking activation of JNK, a proapoptotic signaling component. Within several minutes after binding to the receptor, PRAs block JNK activation induced by tumor necrosis factor-alpha (TNF alpha). The activation of JNK by TNF alpha is another well known mechanism for TNF alpha-induced, as well as other proinflammatory cytokine-induced apoptosis. The method can be used for inhibiting apoptosis which is caspase-mediated or induced by a proinflammatory cytokine, for example TNF alpha or interferon-gamma. It can be used for inhibiting apoptosis associated with a disorder such as e.g. rheumatoid arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac infarction, congestive heart failure, multiple sclerosis, acute disseminated inflammatory leukoencephalitis, progressive multifocal leukoencephalitis, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, ischemic heart disease, Guillain-Barre disease, traumatic brain injury, traumatic spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV, neuropathy, inflammatory neurodegenerative disease, and toxin-induced liver disease. This peptide corresponds to amino acids 8 to 29 of human saposin C (See AAW85653) and acts as a prosaposin receptor agonist.

XX SQ Sequence 22 AA;

Query Match 52.6%; Score 111; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 15
AAB67305
ID AAB67305 standard; Peptide; 22 AA.

XX AC AAB67305;

XX DT 20-APR-2001 (first entry)

XX DE Peptide #5.

XX KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

OS Homo sapiens.
XX PN EP1072609-A2.
XX PD 31-JAN-2001.
XX PF 30-JUN-2000; 2000EP-0305504.
XX PR 30-JUN-1999; 99JP-0185155.
XX PA (SAKA/) SAKANAKA M.
PA (TANA/) TANAKA J.
PA (SATO/) SATO K.
XX PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;
XX DR WPI; 2001-204263/21.
XX PT Use of prosaposin-related peptides or derivatives as cytoprotective agents, for suppressing apoptosis or apoptosis-like cell death -
XX PS Disclosure; Page 28; 41pp; English.
XX CC The present invention relates to use of a prosaposin-related peptide or derivative, in the production of a medicament for use in preventing or delaying cell death, or in promoting the expression of cell death supporting gene product Bcl-XL. The invention is useful for preventing the death of cells e.g. brain cells, neurons and cardiac muscle cells, in vitro or ex vivo.

XX SQ Sequence 22 AA;

Query Match 52.6%; Score 111; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

Search completed: June 2, 2003, 14:15:44
Job time : 32.2821 secs

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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 14.359 Seconds
(without alignments)
267.803 Million cell updates/sec

Title: US-09-780-438C-1
Perfect score: 211
Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	211	100.0	527	1	SAHUP	saposin precursor
2	172	81.5	80	2	S21770	saposin-C - bovine
3	119	56.4	81	2	A32026	glucosylceramide b
4	93	44.1	554	1	A28716	saposin precursor
5	85	40.3	557	1	JH0604	saposin precursor
6	80	37.9	496	2	JS0732	aspartic proteinas
7	78	37.0	428	2	S47096	cynarase (EC 3.4.2
8	78	37.0	474	2	T12049	cyprosin (EC 3.4.2
9	78	37.0	965	2	T00207	PI09 protein - sil
10	75	35.5	508	2	S19697	aspartic proteinas
11	74	35.1	280	2	PC4080	aspartic proteinas
12	74	35.1	506	2	T07915	probable aspartic
13	74	35.1	513	2	T11686	aspartic proteinas
14	72	34.1	292	2	T14446	aspartic proteinas
15	72	34.1	322	2	S41400	aspartic proteinas
16	70	33.2	506	2	F86253	hypothetical prote
17	69	32.7	509	2	S66516	oryzasin (EC 3.4.2
18	69	32.7	509	2	S49349	cyprosin (EC 3.4.2
19	68	32.2	513	2	T09739	aspartic endopepti
20	67.5	32.0	314	2	T15674	hypothetical prote
21	65	30.8	509	2	JC7272	aspartic proteinas
22	64	30.3	3228	2	T21381	hypothetical prote
23	63.5	30.1	330	2	B71625	rifin PFB0040c - m
24	63	29.9	123	2	S75382	hypothetical prote
25	62.5	29.6	139	2	F97080	transcription regu
26	62.5	29.6	226	2	G96975	hypothetical prote
27	62	29.4	213	2	T46069	hypothetical prote
28	61	28.9	506	2	S71591	aspartic proteinas
29	58.5	27.7	1732	2	G84664	hypothetical prote

30	58	27.5	137	2	B64411	hypothetical prote
31	57.5	27.3	209	2	A71800	hypothetical prote
32	57.5	27.3	217	2	T48201	hypothetical prote
33	57	27.0	332	2	T00657	hypothetical prote
34	57	27.0	428	2	D64615	hypothetical prote
35	57	27.0	845	2	D97163	cation transport p
36	56.5	26.8	155	2	C64718	conserved hypothet
37	56.5	26.8	261	2	E85439	thiol-disulfide in
38	56.5	26.8	375	2	A71625	rifin PFB0035c - m
39	56.5	26.8	774	2	JC2299	cell surface glyco
40	56.5	26.8	1048	2	C86189	protein T25N20.11
41	56	26.5	281	2	A97017	uncharacterized pr
42	56	26.5	869	2	F97126	mismatch repair pr
43	56	26.5	1232	2	T47993	hypothetical prote
44	55.5	26.3	1232	2	D64413	cobalamin biosynth
45	55	26.1	105	2	F71128	hypothetical prote

ALIGNMENTS

RESULT 1

SAHUP

saposin precursor [validated] - human

N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon
ein (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 17-Nov-1995 #text_change 08-Dec-2000
C;Accession: JX0061; A57368; A42003; B42003; C42003; D42003; S36140; S36140;
0226; I37265; I37264

R;Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.

J. Biochem. 105, 152-154, 1989

A;Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-gluc
A;Reference number: JX0061; MUID:89255151; PMID:2498298

A;Accession: JX0061

A;Molecule type: mRNA

A;Residues: 1-527 <NAK>

A;Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064

A;Note: alternative splice form 1

A;Accession: A57368

A;Molecule type: mRNA

A;Residues: 1-259,263-527 <NA2>

A;Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756

A;Note: alternative splice form 2

R;Rorman, E.G.; Scheinker, V.; Grabowski, G.A.

Genomics 13, 312-318, 1992

A;Title: Structure and evolution of the human prosaposin chromosomal gene.

A;Reference number: A42003; MUID:92307663; PMID:1612590

A;Accession: A42003

A;Molecule type: DNA

A;Residues: 50-140 <ROR>

A;Cross-references: GB:M86181

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)

A;Accession: B42003

A;Molecule type: DNA

A;Residues: 185-259;263-276 <RO2>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)

A;Accession: C42003

A;Molecule type: DNA

A;Residues: 305-393 <RO3>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence

A;Accession: D42003

A;Molecule type: DNA

A;Residues: 399-487 <RO4>

A;Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence

R;Rorman, E.G.; Grabowski, G.A.

Genomics 5, 486-492, 1989

A;Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sp

A;Reference number: A30367; MUID:90129043; PMID:2515150

A;Accession: A30367

A;Molecule type: mRNA

A;Residues: 1-259,263-527 <RO5>

A;Cross-references: GB:J03077; NID:9183230; PIDN:AAA52560.1; PID:g183231
A;Note: alternative splice form 2
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993
A;Title: Isolation, Characterization, and proteolysis of human prosaposin, the precursor
A;Reference number: S34740; MUID:93311991; PMID:8323276
A;Accession: S34740
A;Molecule type: protein
A;Residues: 17-24;165-172;180-189;301-305 <HIR>
R;Tynnelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.
A;Reference number: S36140; MUID:93380576; PMID:8370464
A;Accession: S36140
A;Molecule type: protein
A;Residues: 'XX',62,'X',64-65,'X',67-79,'X',81-84 <TVY>
A;Note: saposin A
A;Accession: S36141
A;Molecule type: protein
A;Residues: 'XXX',413-414,'X',416-428,'X',430-434 <TY2>
A;Note: saposin D
R;Holtschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7556-7560, 1991
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and
A;Reference number: S36988; MUID:91210267; PMID:2019586
A;Accession: S36988
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-259,263-527 <HOL>
A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative splicing
A;Accession: S36989
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-259,263-527 <HO2>
A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative splicing
A;Accession: S36990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-240,'S',242-259,261-527 <HO3>
A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative splicing
R;Kondoh, K.; Hinenio, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991
A;Title: Isolation and characterization of prosaposin from human milk.
A;Reference number: PS0330; MUID:92068206; PMID:1958198
A;Accession: PS0330
A;Molecule type: protein
A;Residues: 17-24,'X',26 <KON>
A;Experimental source: milk
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation
A;Reference number: A35985; MUID:90207231; PMID:2320574
A;Accession: A35985
A;Molecule type: mRNA
A;Residues: 213-221 <KRE>
A;Cross-references: GB:M32221
A;Accession: B35985
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-259,263-527 <KR2>
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762
A;Experimental source: lymphoblast
A;Accession: C35985
A;Molecule type: mRNA
A;Residues: 213-216,'I',218-221 <KR3>
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; the
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein
A;Reference number: S13195; MUID:91006165; PMID:2209618
A;Accession: S13196
A;Molecule type: protein
A;Residues: 195-259,263-277 <FUE>
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989
A;Title: Saposin A: second cerebroside activator protein.
A;Reference number: A32784; MUID:89240739; PMID:2717620
A;Accession: A32784
A;Molecule type: protein
A;Residues: 60-84;86-107;109-119;125-134 <MOR>
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene
A;Reference number: A41240; MUID:88321660; PMID:2842863
A;Accession: A41240
A;Molecule type: mRNA
A;Residues: 'GSSR',18-259,263-299,'D',301-302,'D',304-527 <OAB>
A;Cross-references: GB:J03086
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein
A;Reference number: S02289; MUID:88068647; PMID:2825202
A;Accession: S02289
A;Status: significant sequence differences
A;Molecule type: mRNA
A;Cross-references: EMBL:J03015
A;Note: this sequence corrected by A41240
A;Note: part of this sequence, including the amino end of the mature protein, was determined
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein
A;Reference number: S02028; MUID:89207118; PMID:3242555
A;Accession: S02028
A;Molecule type: protein
A;Residues: 195-259,263-276 <KLE>
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988
A;Title: The precursor of sulfatide activator protein is processed to three different
A;Reference number: S00813; MUID:89000190; PMID:3048308
A;Accession: S00813
A;Molecule type: protein
A;Residues: 410-487 <FU2>
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurring
A;Reference number: S00226; MUID:88163077; PMID:3442600
A;Accession: S00226
A;Molecule type: protein
A;Residues: 314-393 <KL2>
R;Vaccaro, A.M.; Salvioli, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia J. Biol. Chem. 270, 9953-9960, 1995
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bonds
A;Reference number: A57297; MUID:95247790; PMID:7730378
A;Contents: annotation; disulfide bonds; glycosylation
R;Holtschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991
A;Title: The organization of the gene for the human cerebroside sulfate activator protein
A;Reference number: I37264; MUID:91192146; PMID:2013321
A;Accession: I37265
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 59-125 <RES>
A;Cross-references: EMBL:X57107; NID:g30234; PIDN:CAA40391.1; PID:g30235
A;Accession: I37264
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 307-516 <RE2>
A;Cross-references: EMBL:X57108; NID:g30232; PIDN:CAA40392.1; PID:g1565257
A;Note: sequence revised relative to PID:g30233 (corrected coding region)
C;Genetics;

A:Gene: GDB:PSAP; GLBA
A:Cross-references: GDB:120366; OMIM:176801
A:Map position: 10q22.1-10q22.1
A:Introns: 83/3; 338/3; 401/1; 453/3; 480/3
A>Note: defects in this gene may cause variant Gaucher disease, variant Tay-Sachs disease
A>Note: list of introns is incomplete

Query Match 100.0%; Score 211; DB 1; Length 527;
Best Local Similarity 100.0%; Pred. No. 5.5e-17;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40

Db 314 SDVYCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 353

RESULT 2

S21770

saposin-C - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S21770

R:Sano, A.; Mizuno, T.; Kondoh, K.; Hinenno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.

Biochim. Biophys. Acta 1120, 75-80, 1992

A:Title: Saposin-C from bovine spleen; complete amino acid sequence and relation between

A:Reference number: S21770; MUID:92207994; PMID:1554743

A:Accession: S21770

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-80 <SAN>

C:Superfamily: saposin; saposin repeat homology

Query Match 81.5%; Score 172; DB 2; Length 80;
Best Local Similarity 75.0%; Pred. No. 3e-13;

Matches 30; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 SDVYCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40

Db 1 ADIYQVCEFLVKEVAKLIDNKNTEKEILDADFDMCKSLP 40

RESULT 3

A32026

glucosylceramide beta-glucosidase activator protein SAP-2 - guinea pig

C:Species: Cavia porcellus (guinea pig)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-May-1996

C:Accession: A32026

R:Sano, A.; Radin, N.S.; Johnson, L.L.; Tarr, G.E.

J. Biol. Chem. 263, 19597-19601, 1988

A:Title: The activator protein for glucosylceramide beta-glucosidase from guinea pig liv

A:Reference number: A32026; MUID:89066787; PMID:3198642

A:Accession: A32026

A:Molecule type: protein

A:Residues: 1-81 <SAN>

C:Superfamily: saposin; saposin repeat homology

F:1-81/Domain: saposin repeat homology <SAP>

Query Match 56.4%; Score 119; DB 2; Length 81;
Best Local Similarity 52.6%; Pred. No. 4.6e-07;

Matches 20; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 3 VYCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40

Db 3 VTCKACEYVVKVMEILIDNKNTEKEILDADFDMCKSLP 40

RESULT 4

A28716

saposin precursor - rat

N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfata

N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A28716
R:Collard, M.W.; Sylvester, S.R.; Tsuruta, J.K.; Griswold, M.D.
Biochemistry 27, 4557-4564, 1988
A:Title: Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by ra
A:Reference number: A28716; MUID:89000647; PMID:3048385
A:Accession: A28716
A:Molecule type: mRNA
A:Residues: 1-554 <COL>
A:Cross-references: GB:M19936; NID:g206904; PIDN:AAA42136.1; PID:g206905
A>Note: parts of this sequence, including the amino end of the mature protein, were d
C:Function:
A:Description: saposins bind sphingolipids, form hydrophilic complexes and make them
A:Pathway: sphingolipid catabolism
A>Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-gluc
A>Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by aryls
A>Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester
C:Superfamily: saposin; saposin repeat homology
C:Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome;
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-554/Product: prosaposin #status predicted <PRO>
F:55-148/Domain: saposin repeat homology <SAP1>
F:60-143/Product: saposin A #status predicted <SAPA>
F:189-280/Domain: saposin repeat homology <SAP2>
F:194-273/Product: saposin B #status predicted <SAB1>
F:306-397/Domain: saposin repeat homology <SAP3>
F:310-389/Product: saposin C #status predicted <SAPC>
F:431-522/Domain: saposin repeat homology <SAP4>
F:437-514/Product: saposin D #status predicted <SAPD>
F:63-138,66-132,94-106,439-512,442-506,470-481/Disulfide bonds: #status predicted
F:80,214,331,456/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:197-270,200-264,229-240,314-387,317-381,345-356/Disulfide bonds: #status predicted

Query Match 44.1%; Score 93; DB 1; Length 554;
Best Local Similarity 36.8%; Pred. No. 0.0034;

Matches 14; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 3 VYCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40

Db 312 IFCQVCQLVMKRLSELIINNATEELLIKLSKACSLLP 349

RESULT 5

JH0604

saposin precursor - mouse

N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon

ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulf

N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JH0604

R:Tsuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.

Biochem. Biophys. Res. Commun. 184, 1266-1272, 1992

A:Title: The primary structure of mouse saposin.

A:Reference number: JH0604; MUID:92272718; PMID:1590788

A:Accession: JH0604

A:Molecule type: mRNA

A:Residues: 1-557 <TSU>

A:Cross-references: GB:S36200; NID:g249386; PIDN:AAB22175.1; PID:g249387

A:Experimental source: liver

C:Function:

A:Description: saposins bind sphingolipids, form hydrophilic complexes and make them

A:Pathway: sphingolipid catabolism

A>Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-gluc

A>Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by aryls

A>Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester

C:Superfamily: saposin; saposin repeat homology

C:Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome;

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-557/Product: prosaposin #status predicted <PRO>

F:55-148/Domain: saposin repeat homology <SAP1>

F:60-143/Product: saposin A #status predicted <SAPA>

F:189-283/Domain: saposin repeat homology <SAP2>

QY 2 DVYCEVCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40
| | | | : | | : | | : | | : | | : | |
Db 163 DAACSACEMAVVWIOSQLRQNMTOERILDYVNELCRIP 201

RESULT 15

S41400
aspartic proteinase (EC 3.4.23.-) - wild cabbage (fragment)
N;Alternate names: aspartyl protease
C;Species: Brassica oleracea (wild cabbage)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 29-Aug-1997
C;Accession: S41400
R;Fujikura, Y.; Karssen, C.M.
submitted to the EMBL Data Library, January 1994
A;Description: Cauliflower cDNA with sequence homology to gastric proteases.
A;Reference number: S41400
A;Accession: S41400
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <FUJ>
A;Cross-references: EMBL:X77260
C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a
C;Superfamily: oryzasin; saposin repeat homology
C;Keywords: aspartic proteinase; hydrolase
F;99-144/Domain: saposin repeat homology #status atypical <SAP1>
F;153-203/Domain: saposin repeat homology #status atypical <SAP2>
F;73/Active site: Asp #status predicted

Query Match 34.1%; Score 72; DB 2; Length 322;
Best Local Similarity 30.8%; Pred. No. 0.56;
Matches 12; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 2 DVYCEVCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40
| | | | : | | : | | : | | : | | : | |
Db 163 DAACSACEMAVVWIOSQLRQNMTOERILDYVNELCRIP 201

Search completed: June 2, 2003, 14:16:19
Job time : 16.359 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:13 ; Search time 7.17949 Seconds
(without alignments)
231.082 Million cell updates/sec

Title: US-09-780-438C-1
Perfect score: 211
Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCKSLP 40

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	100.0	524	1	SAP_HUMAN
2	175	82.9	525	1	SAP_BOVIN
3	119	56.4	81	1	SAP_CAVPO
4	108	51.2	518	1	SAP_CHICK
5	93	44.1	554	1	SAP_RAT
6	85	40.3	557	1	SAP_MOUSE
7	80	37.9	496	1	ASPR_ORYSA
8	75	35.5	508	1	ASPR_HORVU
9	69	32.7	509	1	APRL_ORYSA
10	68	32.2	513	1	ASPR_CUCPE
11	64	30.3	473	1	CYPL_CYNCA
12	58.5	27.7	495	1	MATK_TORCL
13	58	27.5	137	1	Y890_METJA
14	57.5	27.3	209	1	YF87_HELPJ
15	56.5	26.8	209	1	YF87_HELPY
16	55	26.1	105	1	Y795_PYRHO
17	55	26.1	313	1	Y085_CABEL
18	55	26.1	389	1	O85C_DROME
19	54	25.6	173	1	ARPL_DROME
20	54	25.6	213	1	KITH_MYCGE
21	53	25.1	196	1	V17_BP7
22	53	25.1	542	1	TCPE_CABEL
23	52.5	24.9	92	1	YA50_HAFIN
24	52	24.6	449	1	ARP3_YEAST
25	51.5	24.4	455	1	VNS1_BMDNV
26	51.5	24.4	524	1	E2BD_MOUSE
27	51.5	24.4	740	1	FAS_PNECA
28	51	24.2	91	1	RR19_NICBI
29	51	24.2	91	1	RR19_TOBAC
30	51	24.2	105	1	YF40_PYRAB
31	51	24.2	129	1	NKL_PIG
32	51	24.2	392	1	MT04_CAMJE
33	51	24.2	453	1	5HT1_APLCA

ALIGNMENTS

RESULT 1

SAP_HUMAN

ID	SAP_HUMAN	STANDARD;	PRT:	524 AA.
AC	P07602; P07292; P15793; P78538; Q92740; Q92739; P78541; P78558;			
DT	01-APR-1988 (Rel. 07, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Proactivator polypeptide precursor [Contains: Saposin A (Protein A); Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside sulfate activator) (CSACT) (Dispersin) (Sulfatide/GM1 activator); Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D (Protein C) (Component C)].			
GN	PSAP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=90129043; PubMed=2515150;			
RA	Rorman E.G., Grabowski G.A.;			
RT	"Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sphingolipid hydrolase activator proteins are encoded by single genes in humans and rats.";			
RT	Genomics 5:486-492(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89255151; PubMed=2498298;			
RA	Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;			
RT	"Structure of full-length cDNA coding for sulfatide activator, a Co-beta-glucosidase and two other homologous proteins: two alternate forms of the sulfatide activator.";			
RT	J. Biochem. 105:152-154(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye, and Skin;			
RA	Strausberg R.;			
RN	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE OF 59-125 AND 304-513 FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=91192146; PubMed=2013321;			
RA	Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D., Suzuki K.;			
RT	"The organization of the gene for the human cerebroside sulfate activator protein.";			
RT	FEBS Lett. 280:267-270(1991).			
RN	[5]			
RP	SEQUENCE OF 164-524 FROM N.A.			
RX	MEDLINE=88068647; PubMed=2825202;			
RA	Dewji N.N., Wenger D.A., O'Brien J.S.;			
RT	"Nucleotide sequence of cloned cDNA for human sphingolipid activator protein 1 precursor.";			

RL Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).
RN [6]
RP PARTIAL SEQUENCE OF 60-142.
RX MEDLINE-89240739; PubMed-2717620;
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,
RA Kishimoto Y.;
RT "Saposin A: second cerebrosidase activator protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).
RN [7]
RP SEQUENCE OF 195-263 FROM N.A.
RX MEDLINE-86130593; PubMed-2868718;
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,
RA Hill F., O'Brien J.S.;
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),
RT the sulfatide-sulfatase activator.";
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).
RN [8]
RP SEQUENCE OF 195-274.
RX TISSUE-Kidney;
RC MEDLINE-91006165; PubMed-2209618;
RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;
RT "The complete amino-acid sequences of human ganglioside GM2 activator
RT protein and cerebrosidase sulfate activator protein.";
RL Eur. J. Biochem. 192:709-714(1990).
RN [9]
RP SEQUENCE OF 195-274.
RX MEDLINE-89207118; PubMed-3242555;
RA Kleinschmidt T., Christomanou H., Braunitzer G.;
RT "Complete amino-acid sequence of the naturally occurring A2 activator
RT protein for enzymic sphingomyelin degradation: identity to the
RT sulfatide activator protein (SAP-1).";
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).
RN [10]
RP SEQUENCE OF 311-390.
RX MEDLINE-88163077; PubMed-3442600;
RA Kleinschmidt T., Christomanou H., Braunitzer G.;
RT "Complete amino-acid sequence and carbohydrate content of the
RT naturally occurring glucosylceramide activator protein (A1 activator)
RT absent from a new human Gaucher disease variant.";
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).
RN [11]
RP SEQUENCE OF 407-484.
RX MEDLINE-89000190; PubMed-3048308;
RA Furst W., Machleidt W., Sandhoff K.;
RT "The precursor of sulfatide activator protein is processed to three
RT different proteins.";
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).
RN [12]
RP PARTIAL SEQUENCE OF 405-484.
RX MEDLINE-89025876; PubMed-2845979;
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;
RT "Saposin D: a sphingomyelinase activator.";
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).
RN [13]
RP SEQUENCE OF 17-26.
RX TISSUE-Milk;
RC MEDLINE-92068206; PubMed-1958198;
RA Kondoh K., Hineno T., Sano A., Kakimoto Y.;
RT "Isolation and characterization of prosaposin from human milk.";
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).
RN [14]
RP PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.
RX TISSUE-Urine;
RC MEDLINE-20032116; PubMed-10562467;
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,
RA Waring A.J., To T., Fluharty C.B., Faull K.F.;
RT "Preparation of the cerebrosidase sulfate activator (CSAct or saposin B)
RT from human urine.";
RL Mol. Genet. Metab. 68:391-403(1999).
RN [15]
RP STRUCTURE OF CARBOHYDRATE ON ASN-215.
RX MEDLINE-21110404; PubMed-11180632;
RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,

RA Stevens R.L., Fluharty C.B., Fluharty A.L.;
RT "Structure of the asparagine-linked sugar chains of porcine kidney and
RT human urine cerebrosidase sulfate activator protein.";
RL J. Mass Spectrom. 35:1416-1424(2000).
RN [16]
RP MASS SPECTROMETRY.
RC TISSUE-Urine;
RX MEDLINE-99441404; PubMed-10510427;
RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,
RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,
RA Fluharty C.B., Fluharty A.L.;
RT "Cerebrosidase sulfate activator protein (Saposin B): chromatographic
RT and electrospray mass spectrometric properties.";
RL J. Mass Spectrom. 34:1040-1054(1999).
RN [17]
RP VARIANT MLD ILE-217.
RX MEDLINE-90147748; PubMed-2302219;
RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;
RT "Detection of a point mutation in sphingolipid activator protein-1
RT mRNA in patients with a variant form of metachromatic
RT leukodystrophy.";
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).
RN [18]
RP SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.
RX MEDLINE-90207231; PubMed-2320574;
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,
RA O'Brien J.S.;
RT "Characterization of a mutation in a family with saposin B
RT deficiency: a glycosylation site defect.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).
RN [19]
RP VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-91210267; PubMed-2019586;
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,
RA Suzuki K.;
RT "Sulfatide activator protein. Alternative splicing that generates
RT three mRNAs and a newly found mutation responsible for a clinical
RT disease.";
RL J. Biol. Chem. 266:7556-7560(1991).
RN [20]
RP VARIANT GAUCHER PHE-388.
RX MEDLINE-91285107; PubMed-2060627;
RA Schnabel D., Schroeder M., Sandhoff K.;
RT "Mutation in the sphingolipid activator protein 2 in a patient with a
RT variant of Gaucher disease.";
RL FEBS Lett. 284:57-59(1991).
RN [21]
RP REVIEW ON MLD VARIANTS.
RX MEDLINE-95170731; PubMed-7866401;
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;
RT "Molecular genetics of metachromatic leukodystrophy.";
RL Hum. Mutat. 4:233-242(1994).
CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place
CC by the sequential action of specific hydrolases. Some of these
CC enzymes require specific low-molecular mass, non-enzymic proteins:
CC the sphingolipids activator proteins (coproteins).
CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).
CC Saposin C apparently acts by combining with the enzyme and acidic
CC lipid to form an activated complex, rather than by solubilizing
CC the substrate.
CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-
CC cerebrosidase sulfate by arylsulfatase A (EC 3.1.6.8), GM1
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).
CC Saposin B forms a solubilizing complex with the substrates of the
CC sphingolipid hydrolases.
CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase
CC activator (EC 3.1.4.12).
CC -!- SUBUNIT: Saposin B is a homodimer.
CC -!- SUBCELLULAR LOCATION: Lysosomal.
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),

Query Match 100.0%; Score 211; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.4e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
|||||
Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 2

SAP_BOVIN STANDARD; PRT; 525 AA.
AC P26779; Q9N2G4;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE proactivator polypeptide precursor [Contains: Saposin A (Protein A);
DE Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside
DE sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);
DE Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase
DE activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D
DE (Protein C) (Component C)].
GN PSAP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC TISSUE=Mammary gland;
RA Azuma N., Yoshida K.;
RT "RT-PCR cloning of bovine prosaposin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 312-391.
RC TISSUE=Spleen;
RX MEDLINE=92207994; PubMed=1554743;
RA Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,
RA Morita N.;
RT "Saposin-C from bovine spleen; complete amino acid sequence and
RT relation between the structure and its biological activity.";
RL Biochim. Biophys. Acta 1120:75-80(1992).
CC -1- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
CC BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
CC ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
CC THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCEAMIDE BY BETA-GALACTOSYLCEAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCEAMIDE BY BETA-GALACTOSYLCEAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE.
CC -1- FUNCTION: SAPOSIN B STIMULATES THE HYDROLYSIS OF GALACTO-
CC CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
CC GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
CC GLOBOTRIACOSYLCEAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).
CC SAPOSIN B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
CC SPHINGOLIPID HYDROLASES (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
CC ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
CC -1- SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Lysosomal.
CC -1- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL
CC PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID
CC HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
CC -----
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DR EMBL; AB036791; BAA95677.1;
DR PIR; S21770; S21770.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 4.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
KW Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 60 142 SAPOSIN A.
FT CHAIN 196 275 SAPOSIN B.
FT CHAIN 312 392 SAPOSIN C.
FT CHAIN 406 487 SAPOSIN D.
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 59 142 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 194 276 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 312 393 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 406 487 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 492 525 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 63 138 BY SIMILARITY.
FT DISULFID 66 132 BY SIMILARITY.
FT DISULFID 94 106 BY SIMILARITY.
FT DISULFID 199 272 BY SIMILARITY.
FT DISULFID 202 266 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 316 389 BY SIMILARITY.
FT DISULFID 319 383 BY SIMILARITY.
FT DISULFID 347 358 BY SIMILARITY.
FT DISULFID 410 483 BY SIMILARITY.
FT DISULFID 413 477 BY SIMILARITY.
FT DISULFID 441 452 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .).
FT CARBOHYD 427 427 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 127 127 H -> R.
FT VARIANT 260 263 MQPK -> IRIR.
FT CONFLICT 317 317 E -> Q (IN REF. 2).
FT CONFLICT 367 367 R -> S (IN REF. 1).
SQ SEQUENCE 525 AA; 58120 MW; 233AFC0FB9C4FA99 CRC64;

Query Match 82.9%; Score 175; DB 1; Length 525;
Best Local Similarity 77.5%; Pred. No. 1.6e-13;
Matches 31; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 312 ADIYCEVCEFLVKEVAKLIDNNRTEELHALDKVCSKLP 351

RESULT 3

SAP_CAVPO STANDARD; PRT; 81 AA.
AC P20097;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Saposin C (CO-beta-glucosidase) (Glucosylceramidase activator)
DE (Sphingolipid activator protein 2) (SAP-2).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;


```
RESULT 5
SAP_RAT      STANDARD;      PRT;      554 AA.
ID  SAP_RAT      STANDARD;      PRT;      554 AA.
AC  P10960; Q62841; Q64190;
DT  01-JUL-1989 (Rel. 11, Created)
DT  01-JUL-1989 (Rel. 11, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
GN  PSAP OR SGPI.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC  TISSUE=Sertoli cells;
RX  MEDLINE=89000647; PubMed=3048385;
RA  Collard M.W., Sylvester S.R., Tsuruta J.K., Griswold M.D.;
RT  "Biosynthesis and molecular cloning of sulfated glycoprotein 1
RT  secreted by rat Sertoli cells: sequence similarity with the
RT  70-kilodalton precursor to sulfatide/GM1 activator.";
RL  Biochemistry 27:4557-4564(1988).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Testis;
RX  MEDLINE=96128541; PubMed=8573994;
RA  Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
RT  "Molecular role of sulfated glycoprotein-1 (SGP-1/prosaposin) in
RT  Sertoli cells.";
RL  Histol. Histopathol. 10:1023-1034(1995).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Testicle;
RX  MEDLINE=96175245; PubMed=8601692;
RA  Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
RT  "Expression and tissue distribution of rat sulfated glycoprotein-1
RT  (prosaposin).";
RL  J. Histochem. Cytochem. 44:327-337(1996).
CC  -1- SUBCELLULAR LOCATION: Extracellular.
CC  -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC  -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
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EMBL; M19936; AAA42136.1; -
EMBL; S81353; AAB36042.2; -
EMBL; S81373; AAB36233.2; -
PIR; A28716; A28716.
InterPro; IPR003119; Sapa.
InterPro; IPR000004; SapB.
Pfam; PF02199; SAPA; 2.
ProDom; PD001732; SapB; 4.
SMART; SM00162; SAPA; 2.
SMART; SM00118; SAPB; 4.
KW  Sulfation; Signal; Glycoprotein; Repeat.
FT  SIGNAL      1 16
FT  CHAIN       17 554      SULFATED GLYCOPROTEIN 1.
FT  DOMAIN      21 54      SAPOSIN-LIKE TYPE A 1.
FT  DOMAIN      61 138      SAPOSIN-LIKE TYPE B 1.
FT  DOMAIN      193 274      SAPOSIN-LIKE TYPE B 2.
FT  DOMAIN      310 391      SAPOSIN-LIKE TYPE B 3.
FT  DOMAIN      435 516      SAPOSIN-LIKE TYPE B 4.
FT  DOMAIN      521 554      SAPOSIN-LIKE TYPE A 2.
FT  DISULFID    63 138      BY SIMILARITY.
FT  DISULFID    66 132      BY SIMILARITY.
FT  DISULFID    94 106      BY SIMILARITY.
FT  DISULFID    197 270      BY SIMILARITY.
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FT  DISULFID    200      BY SIMILARITY.
FT  DISULFID    229      BY SIMILARITY.
FT  DISULFID    314      BY SIMILARITY.
FT  DISULFID    317      BY SIMILARITY.
FT  DISULFID    345      BY SIMILARITY.
FT  DISULFID    439      BY SIMILARITY.
FT  DISULFID    442      BY SIMILARITY.
FT  DISULFID    470      BY SIMILARITY.
FT  CARBOHYD     80      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    214      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    331      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    456      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CONFLICT    115      P -> L (IN REF. 2 AND 3).
FT  CONFLICT    299      D -> E (IN REF. 2).
FT  CONFLICT    462      I -> V (IN REF. 3).
FT  CONFLICT    527      W -> R (IN REF. 3).
FT  CONFLICT    536      S -> M (IN REF. 3).
SQ  SEQUENCE    554 AA; 61123 MW; DFE3F3A3A0520C6B CRC64;
Query Match      44.1%; Score 93; DB 1; Length 554;
Best Local Similarity 36.8%; Pred. No. 0.00091;
Matches 14; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY  3 VYCEVCEFLVKEVTKLIDNKNTEKEILDADFDMCKSLP 40
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db  312 IFCQVCQLVMRKLSELIINNATEELLIKGLSKACSLLP 349

RESULT 6
SAP_MOUSE      STANDARD;      PRT;      557 AA.
ID  SAP_MOUSE      STANDARD;      PRT;      557 AA.
AC  Q61207; Q64219; Q64006; Q60861;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
GN  PSAP OR SGPI.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver;
RX  MEDLINE=92272718; PubMed=1590788;
RA  Tsuda M., Sakiyama T., Endo H., Kitagawa T.;
RT  "The primary structure of mouse saaposin.";
RL  Biochem. Biophys. Res. Commun. 184:1266-1272(1992).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=94272317; PubMed=8003952;
RA  Sprecher-Levy H., Orr-Urtreger A., Lonai P., Horowitz M.;
RT  "Murine prosaposin: expression in the reproductive system of a gene
RT  implicated in human genetic disease.";
RL  Cell. Mol. Biol. 40:233-233(1994).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=96084310; PubMed=8565332;
RA  Cao Q.P., Crain W.R.;
RT  "Expression of SGP-1 mRNA in preimplantation mouse embryos.";
RL  Dev. Genet. 17:263-271(1995).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c; TISSUE=Liver;
RA  Zhao Q.Q., Hay N.N., Morales C.R.;
RL  Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC  -1- SUBCELLULAR LOCATION: Extracellular.
CC  -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC  -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
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RN [1] SEQUENCE FROM N.A.
 RC STRAIN=cv. Kustaa; TISSUE=Embryo;
 RX MEDLINE=92111473; PubMed=1722454;
 RA Runeberg-Roos P., Toermaekangas K., Oestman A.;
 RT "Primary structure of a barley-grain aspartic proteinase. A plant
 aspartic proteinase resembling mammalian cathepsin D.";
 RL Eur. J. Biochem. 202:1021-1027(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=cv. Kustaa; TISSUE=Embryo;
 RX MEDLINE=92254717; PubMed=1812727;
 RA Toermaekangas K., Runeberg-Roos P., Oestman A., Tilgmann C.;
 RA Sarkkinen P., Kervinen J., Mikola L., Kalkkinen N.;
 RT "Aspartic proteinase from barley seeds is related to animal cathepsin
 D.";
 RL Adv. Exp. Med. Biol. 306:355-359(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=99335466; PubMed=10406799;
 RA Kervinen J., Tobin G.J., Costa J., Waugh D.S., Wlodawer A., Zdanov A.;
 RT "Crystal structure of plant aspartic proteinase prophylpsin:
 inactivation and vacuolar targeting";
 RL EMBO J. 18:3947-3955(1999).
 CC -1- CATALYTIC ACTIVITY: Prefers hydrophobic residues Phe, Val, Ile,
 Leu, and Ala at P1 and P1', but also cleaves -Phe-|-Asp- and
 -Asp-|-Asp- bonds in 2S albumin from plants seeds.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS (29 kDa AND 11 kDa) PROCESSED
 FROM THE PRECURSOR MOLECULE. A LARGE ENZYME (32 kDa AND 16 kDa) IS
 AN INTERMEDIATE PRECURSOR FORM.
 CC -1- SUBCELLULAR LOCATION: Vacuolar.
 CC -1- TISSUE SPECIFICITY: EMBRYO AND LEAF.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 CC -----
 DR EMBL; X56136; CAA39602.1; -.
 DR PDB; 1QDM; 16-JUL-99.
 DR MEROPS; A01.020; -.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR InterPro; IPR000004; SapB.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR ProDom; PD001732; SapB; 1.
 DR SMART; SM00118; SAPB; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR Hydrolase; Aspartyl protease; Zymogen; Glycoprotein; Signal;
 KW 3D-structure. 1 22 POTENTIAL.
 FT SIGNAL 1 22
 FT PROPEP 23 66
 FT CHAIN 67 377
 FT CHAIN 67 ?
 FT CHAIN 378 508
 FT CHAIN 422 508
 FT CHAIN 317 420
 FT DOMAIN 377 378
 FT SITE 421 422
 FT SITE 102 102
 FT ACT_SITE 289 289
 FT DISULFID 115 121
 FT DISULFID 280 284
 FT DISULFID 427 464
 FT CARBOHYD 399 399
 FT SEQUENCE 508 AA; 54226 MW; 87F2C9F93369B962 CRC64;
 SQ SEQUENCE 508 AA; 54226 MW; 87F2C9F93369B962 CRC64;
 Query Match 35.5%; Score 75; DB 1; Length 508;
 Best Local Similarity 36.1%; Pred. No. 0.58;
 Matches 13; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

Best Local Similarity 35.0%; Pred. No. 0.11;
 Matches 14; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
 QY 1 SDVYCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40
 Db 378 ADPMCSACEMAVVMQNLQAKNTQDLIDYVNLNRLP 417
 RESULT 9
 APR1_ORYSA STANDARD; PRT; 509 AA.
 ID APR1_ORYSA
 AC Q42456;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartic proteinase oryzasin 1 precursor (EC 3.4.23.-).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare / Japonica; TISSUE=Seed;
 RX MEDLINE=96048031; PubMed=7556174;
 RA Asakura T., Watanabe H., Abe K., Arai S.;
 RT "Rice aspartic proteinase, oryzasin, expressed during seed ripening
 and germination, has a gene organization distinct from those of
 animal and microbial aspartic proteinases";
 RL Eur. J. Biochem. 232:77-83(1995).
 CC -1- DEVELOPMENTAL STAGE: SEED RIPENING AND GERMINATION.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D32165; BAA06876.1; -.
 DR EMBL; D32144; BAA06875.1; -.
 DR HSSP; P42210; IQDM.
 DR MEROPS; A01.020; -.
 DR InterPro; IPR001461; AspproteaseA1.
 DR InterPro; IPR001969; Aspprotease_site.
 DR InterPro; IPR000004; SapB.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR ProDom; PD001732; SapB; 1.
 DR SMART; SM00118; SAPB; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR Hydrolase; Aspartyl protease; Zymogen; Glycoprotein; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 67
 FT CHAIN 68 509
 FT DOMAIN 318 416
 FT ACT_SITE 103 103
 FT ACT_SITE 290 290
 FT DISULFID 116 122
 FT DISULFID 281 285
 FT DISULFID 428 465
 FT CARBOHYD 252 252
 FT CARBOHYD 400 400
 FT SEQUENCE 509 AA; 54145 MW; 182F5DADA4CBE358 CRC64;
 SQ SEQUENCE 509 AA; 54145 MW; 182F5DADA4CBE358 CRC64;
 Query Match 32.7%; Score 69; DB 1; Length 509;
 Best Local Similarity 36.1%; Pred. No. 0.58;
 Matches 13; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKILDAFDKMSKLP 40
 Query Match 32.7%; Score 69; DB 1; Length 509;
 Best Local Similarity 36.1%; Pred. No. 0.58;
 Matches 13; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 26.1538 Seconds
(without alignments)
315.131 Million cell updates/sec

Title: US-09-780-438C-1
Perfect score: 211
Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*

- ```

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Query Length | DB Length | ID     | Description         |
|------------|-------|-------|--------------|-----------|--------|---------------------|
| 1          | 94    | 44.5  | 294          | 5         | Q95X03 | Q95x03 naegleria f  |
| 2          | 94    | 44.5  | 307          | 5         | Q9BKM2 | Q9bkm2 naegleria f  |
| 3          | 92    | 43.6  | 520          | 13        | Q8UVZ4 | Q8uvz4 brachydanio  |
| 4          | 92    | 43.6  | 522          | 13        | Q9DC82 | Q9dgc82 brachydanio |
| 5          | 84    | 39.8  | 200          | 5         | Q8T213 | Q8t213 dictyosteli  |
| 6          | 79    | 37.4  | 517          | 10        | O81654 | O81654 hemerocalli  |
| 7          | 78    | 37.0  | 965          | 5         | O15997 | O15997 bombyx mori  |
| 8          | 77    | 36.5  | 514          | 10        | Q9FRW8 | Q9frw8 nepenthes a  |
| 9          | 75    | 35.5  | 495          | 10        | Q9LGZ3 | Q9lgz3 oryza sativ  |
| 10         | 74    | 35.1  | 273          | 10        | Q9LUX5 | Q9lux5 pyrus pyrif  |
| 11         | 74    | 35.1  | 506          | 10        | Q39311 | Q39311 brassica na  |
| 12         | 74    | 35.1  | 513          | 10        | Q41713 | Q41713 vigna ungui  |
| 13         | 74    | 35.1  | 514          | 10        | Q9FRW9 | Q9frw9 nepenthes a  |
| 14         | 73    | 34.6  | 456          | 5         | O94472 | O94472 dictyosteli  |
| 15         | 73    | 34.6  | 953          | 5         | Q9Y125 | Q9y125 drosophila   |
| 16         | 72    | 34.1  | 292          | 10        | Q43407 | Q43407 brassica ol  |

|    |      |      |      |    |        |                    |
|----|------|------|------|----|--------|--------------------|
| 17 | 70   | 33.2 | 486  | 10 | Q38934 | Q38934 arabidopsis |
| 18 | 70   | 33.2 | 506  | 10 | Q65390 | Q65390 arabidopsis |
| 19 | 69   | 32.7 | 441  | 5  | Q9U9P3 | Q9U9P3 drosophila  |
| 20 | 69   | 32.7 | 509  | 10 | Q96383 | Q96383 centaurea c |
| 21 | 69   | 32.7 | 509  | 10 | Q39476 | Q39476 cynara card |
| 22 | 68   | 32.2 | 514  | 10 | Q94IA2 | Q94IA2 glycine max |
| 23 | 67.5 | 32.0 | 238  | 5  | Q18276 | Q18276 caenorhabdi |
| 24 | 67   | 31.8 | 507  | 10 | Q9FRW7 | Q9FRW7 nepenthes a |
| 25 | 65   | 30.8 | 509  | 10 | Q9SSZ1 | Q9SSZ1 helianthus  |
| 26 | 64   | 30.3 | 1601 | 5  | Q9NDH1 | Q9NDH1 caenorhabdi |
| 27 | 63.5 | 30.1 | 330  | 5  | Q96114 | Q96114 plasmodium  |
| 28 | 63   | 29.9 | 123  | 17 | P95954 | P95954 sulfolobus  |
| 29 | 63   | 29.9 | 143  | 5  | Q76179 | Q76179 dictyosteli |
| 30 | 63   | 29.9 | 159  | 10 | Q94KV2 | Q94KV2 manihot esc |
| 31 | 63   | 29.9 | 458  | 5  | Q95X02 | Q95X02 naegleria f |
| 32 | 63   | 29.9 | 484  | 5  | Q9BKM1 | Q9BKM1 naegleria f |
| 33 | 63   | 29.9 | 506  | 10 | Q9XFX4 | Q9XFX4 cynara card |
| 34 | 63   | 29.9 | 513  | 10 | Q8VYL3 | Q8VYL3 arabidopsis |
| 35 | 62.5 | 29.6 | 139  | 16 | Q97J21 | Q97J21 clostridium |
| 36 | 62.5 | 29.6 | 226  | 16 | Q97LE5 | Q97LE5 clostridium |
| 37 | 62.5 | 29.6 | 1204 | 4  | Q9BZV5 | Q9BZV5 homo sapien |
| 38 | 62.5 | 29.6 | 1204 | 4  | Q9HAV4 | Q9HAV4 homo sapien |
| 39 | 62   | 29.4 | 213  | 10 | Q9SCT5 | Q9SCT5 arabidopsis |
| 40 | 62   | 29.4 | 504  | 8  | Q9MVV8 | Q9MVV8 taxus bacca |
| 41 | 61   | 28.9 | 174  | 10 | Q9M614 | Q9M614 vitis ripar |
| 42 | 61   | 28.9 | 506  | 10 | Q40140 | Q40140 lycopersico |
| 43 | 60   | 28.4 | 469  | 8  | Q9BB23 | Q9BB23 blfrenaria  |
| 44 | 60   | 28.4 | 505  | 10 | Q9FRW6 | Q9FRW6 nepenthes a |
| 45 | 60   | 28.4 | 510  | 8  | Q9MVV5 | Q9MVV5 taxus chine |

## ALIGNMENTS

```

RESULT 1
Q95X03
ID Q95X03 PRELIMINARY; PRT; 294 AA.
AC Q95X03;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Naegleriapore A (Fragment).
GN NP-A.
OS Naegleria fowleri.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae
OX NCBI_TaxID=5763;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickel R., Leippe M.;
RT "Pore-forming peptides of Naegleria fowleri.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF196308; AAL01157.1; -.
DR InterPro; IPR000004; SapB.
DR ProDom; PD001732; SapB; 2.
FT NON_TER 1
SQ SEQUENCE 294 AA; 31895 MW; 0B67550766B5B1D8 CRC64;

Query Match 44.5%; Score 94; DB 5; Length 29
Best Local Similarity 35.9%; Pred. No. 0:0026;
Matches 14; Conservative 13; Mismatches 12; Indels

QY 2 DVYCEVCEFLVKEVTKLIDNNKTEKEILDADFKNCKSLP 40
| | | | | | | | | | | | | | | | | | | |
Db 104 DAECEICKFVIOQVEAFIESNHSQAEIQKELNKLCSVP 142

RESULT 2
Q9BK02
ID Q9BK02 PRELIMINARY; PRT; 307 AA.
AC Q9BK02;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

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DE Naegleriapore A pore-forming peptide.
GN PRNP-A.
OS Naegleria fowleri.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
OX NCBI_TaxID=5763;
RN [1]
RP SEQUENCE FROM N.A.
RA Nickel R., Benkert C., Jacobs T., Marti T., Marciano-Cabral F.,
RA Leippe M.;
RT "Pore-forming peptides of Naegleria fowleri.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154046; AAK21658.1; -.
DR InterPro; IPR000004; SapB.
DR ProDom; PD001732; SapB; 2.
DR SMART; SM00118; SAPB; 3.
SQ SEQUENCE 307 AA; 33133 MW; 8503E4A755BC6DDF CRC64;

Query Match 44.5%; Score 94; DB 5; Length 307;
Best Local Similarity 35.9%; Pred. No. 0.0027;
Matches 14; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 2 DVYCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
Db 117 DAECEICKFVIQQVEAFIESNHSQAEIQKELNKLCSVP 155

RESULT 3
Q8UVZ4
ID Q8UVZ4 PRELIMINARY; PRT; 520 AA.
AC Q8UVZ4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Lysosomal cofactor/neutrotrophic factor prosaposin.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Seo H.-C., Lie O., Fjose A., O'Brien J.S., Kishimoto Y.;
RT "Cloning, expression and promoter analysis of zebrafish prosaposin.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF276996; AAL54381.1; -.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 3.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
SQ SEQUENCE 520 AA; 57431 MW; F9E620F84BA41CB5 CRC64;

Query Match 43.6%; Score 92; DB 13; Length 520;
Best Local Similarity 38.9%; Pred. No. 0.0076;
Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
Db 312 CAICEYVMKEIENMIQDQTSAEIVQAVEKVCNLLP 347

RESULT 4
Q9DG82
ID Q9DG82 PRELIMINARY; PRT; 522 AA.
AC Q9DG82;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Prosaposin.
GN PSAP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Altman N., Horowitz M.;
RT "The zebrafish prosaposin cDNA.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108655; AAG32919.1; -.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR InterPro; IPR003119; SapA.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 3.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
SQ SEQUENCE 522 AA; 57671 MW; D3C15A305725C1CD CRC64;

Query Match 43.6%; Score 92; DB 13; Length 522;
Best Local Similarity 38.9%; Pred. No. 0.0076;
Matches 14; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
Db 314 CAICEYVMKEIENMIQDQTSAEIVQAVEKVCNLLP 349

RESULT 5
Q8T2L3
ID Q8T2L3 PRELIMINARY; PRT; 200 AA.
AC Q8T2L3;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Proteasome subunit beta type 1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelidida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115596; AAL92313.1; -.
SQ SEQUENCE 200 AA; 22473 MW; 89DDB0520BDFA407 CRC64;

Query Match 39.8%; Score 84; DB 5; Length 200;
Best Local Similarity 41.7%; Pred. No. 0.027;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
Db 23 CELCQFSVKAEDLVQNTQSQIIPYLDACSLLP 58

RESULT 6
O81654
ID O81654 PRELIMINARY; PRT; 517 AA.
AC O81654;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Senescence-associated protein 4.
GN SA4.
OS Hemerocallis hybrid cultivar.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
OC Hemerocallidaceae; Hemerocallis.
OX NCBI_TaxID=80862;
RN [1]
```









|    |                                                          |
|----|----------------------------------------------------------|
| RA | Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., |
| RA | Park S., Sequeira A., Sethi H., Snir E., Svirska R.R.,   |
| RA | Celniker S.E.;                                           |
| RT | "Full length Drosophila melanogaster cDNA sequence.";    |
| RL | Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  |
| DR | EMBL; AE003775; AAF57097.1; -.                           |
| DR | EMBL; AF145647; AAD38622.1; -.                           |
| DR | FlyBase; FBgn0000416; Sap-r.                             |
| DR | InterPro; IPR03119; SapA.                                |
| DR | InterPro; IPR00004; SapB.                                |
| DR | Pfam; PF02199; SAPA; 1.                                  |
| DR | proDom; PD001732; SapB; 6.                               |
| DR | SMART; SM00162; SAPA; 1.                                 |
| DR | SMART; SM00118; SAPB; 7.                                 |
| SQ | SEQUENCE 953 AA; 105962 MW; D6CFFD3E9D1502A8 CRC64;      |

Query Match 34.6%; Score 73; DB 5; Length 953;  
Best Local Similarity 27.5%; Pred. NO. 2.3;  
Matches 11; Conservative 13; Mismatches 16; Indels

QY                1 SDVYCEVFCEFLKYEVTKLIDNNKTEKEILDAFDMCSKLIP 40  
                : | : : : : : : : : : : : : : : : : :  
Db              68 TDSICTICKMVTQARDQLKSQTTEEELKEVFEGGSKLIP 107

Search completed: June 2, 2003, 14:17:17  
Job time : 28.6538 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:43 ; Search time 12.3077 Seconds  
(without alignments)  
95.624 Million cell updates/sec

Title: US-09-780-438C-1  
Perfect score: 211  
Sequence: 1 SDVCEVCEFLVKEVTKLIDNNKTEKEILDAFDKMCCKLP 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Length | DB ID | Description       |
|------------|-------|---------|--------|-------|-------------------|
| 1          | 211   | 100.0   | 80     | 1     | US-08-100-247-3   |
| 2          | 211   | 100.0   | 80     | 1     | US-08-483-146A-3  |
| 3          | 211   | 100.0   | 80     | 1     | US-08-232-513A-4  |
| 4          | 211   | 100.0   | 80     | 1     | US-08-484-594A-3  |
| 5          | 211   | 100.0   | 523    | 1     | US-08-100-247-2   |
| 6          | 211   | 100.0   | 523    | 1     | US-08-483-146A-2  |
| 7          | 211   | 100.0   | 523    | 1     | US-08-232-513A-3  |
| 8          | 211   | 100.0   | 523    | 1     | US-08-484-594A-2  |
| 9          | 111   | 52.6    | 22     | 1     | US-08-100-247-1   |
| 10         | 111   | 52.6    | 22     | 1     | US-08-483-146A-1  |
| 11         | 111   | 52.6    | 22     | 1     | US-08-232-513A-1  |
| 12         | 111   | 52.6    | 22     | 1     | US-08-484-594A-1  |
| 13         | 111   | 52.6    | 22     | 4     | US-09-231-159-1   |
| 14         | 111   | 52.6    | 22     | 4     | US-08-611-307-1   |
| 15         | 111   | 52.6    | 22     | 4     | US-09-148-030-1   |
| 16         | 106   | 50.2    | 22     | 4     | US-09-231-159-8   |
| 17         | 106   | 50.2    | 22     | 4     | US-08-611-307-8   |
| 18         | 96    | 45.5    | 22     | 1     | US-08-483-146A-9  |
| 19         | 96    | 45.5    | 22     | 1     | US-08-232-513A-18 |
| 20         | 96    | 45.5    | 22     | 1     | US-08-484-594A-9  |
| 21         | 96    | 45.5    | 22     | 4     | US-09-231-159-7   |
| 22         | 96    | 45.5    | 22     | 4     | US-08-611-307-7   |
| 23         | 83    | 39.3    | 18     | 1     | US-08-100-247-5   |
| 24         | 83    | 39.3    | 18     | 1     | US-08-483-146A-5  |
| 25         | 83    | 39.3    | 18     | 1     | US-08-232-513A-6  |
| 26         | 83    | 39.3    | 18     | 1     | US-08-484-594A-5  |
| 27         | 83    | 39.3    | 18     | 4     | US-09-231-159-20  |

|    |      |      |     |   |                     |                   |
|----|------|------|-----|---|---------------------|-------------------|
| 28 | 83   | 39.3 | 18  | 4 | US-08-611-307-20    | Sequence 20, Appl |
| 29 | 83   | 39.3 | 18  | 4 | US-09-148-030-2     | Sequence 2, Appl  |
| 30 | 75   | 35.5 | 15  | 4 | US-09-148-030-10    | Sequence 10, Appl |
| 31 | 75   | 35.5 | 22  | 1 | US-08-483-146A-8    | Sequence 8, Appl  |
| 32 | 75   | 35.5 | 22  | 1 | US-08-232-513A-17   | Sequence 17, Appl |
| 33 | 75   | 35.5 | 22  | 1 | US-08-484-594A-8    | Sequence 8, Appl  |
| 34 | 75   | 35.5 | 22  | 4 | US-09-231-159-6     | Sequence 6, Appl  |
| 35 | 75   | 35.5 | 22  | 4 | US-08-611-307-6     | Sequence 6, Appl  |
| 36 | 64   | 30.3 | 14  | 4 | US-09-231-159-9     | Sequence 9, Appl  |
| 37 | 64   | 30.3 | 14  | 4 | US-08-611-307-9     | Sequence 9, Appl  |
| 38 | 63   | 29.9 | 14  | 4 | US-09-231-159-10    | Sequence 10, Appl |
| 39 | 63   | 29.9 | 14  | 4 | US-08-611-307-10    | Sequence 10, Appl |
| 40 | 63   | 29.9 | 15  | 4 | US-09-148-030-9     | Sequence 9, Appl  |
| 41 | 59   | 28.0 | 12  | 4 | US-09-231-159-3     | Sequence 3, Appl  |
| 42 | 59   | 28.0 | 12  | 4 | US-08-611-307-3     | Sequence 3, Appl  |
| 43 | 59   | 28.0 | 12  | 4 | US-09-148-030-3     | Sequence 3, Appl  |
| 44 | 57.5 | 27.3 | 388 | 4 | US-09-134-001C-3820 | Sequence 3820, Ap |
| 45 | 55   | 26.1 | 78  | 2 | US-08-732-228-1     | Sequence 1, Appl  |

ALIGNMENTS

RESULT 1  
US-08-100-247-3  
; Sequence 3, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: OBRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; CLONE: SAPOSIN C  
; US-08-100-247-3

Query Match 100.0%; Score 211; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. NO. 2.1e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||  
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

## RESULT 2

US-08-483-146A-3

; Sequence 3, Application US/08483146A  
; Patent No. 5696080

; GENERAL INFORMATION:

; APPLICANT: O'Brien, John S.

; APPLICANT: Kishimoto, Yasuo

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED

; TITLE OF INVENTION: THEREFROM

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson and Bear

; STREET: 620 Newport Center Blvd. 16th Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/483,146A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Israelsen, Ned A

; REGISTRATION NUMBER: 29,655

; REFERENCE/DOCKET NUMBER: MYELOS.002DV1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-235-8550

; TELEFAX: 619-235-0176

; TELEX:

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

US-08-483-146A-3

Query Match 100.0%; Score 211; DB 1; Length 80;

Best Local Similarity 100.0%; Pred. No. 2.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
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Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||

## RESULT 3

US-08-232-513A-4

; Sequence 4, Application US/08232513A

; Patent No. 5700909

; GENERAL INFORMATION:

; APPLICANT: O'Brien, John S.

; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides

; TITLE OF INVENTION: as Therapeutic Agents

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell &amp; Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,513A

; FILING DATE: 21-APR-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/100,247

; FILING DATE: 30-JUL-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-UD 1643

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 80 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..80

; OTHER INFORMATION: /label= Saposin\_C

US-08-232-513A-4

Query Match 100.0%; Score 211; DB 1; Length 80;

Best Local Similarity 100.0%; Pred. No. 2.1e-20;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||

Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||

## RESULT 4

US-08-484-594A-3

; Sequence 3, Application US/08484594A

; Patent No. 5714459

; GENERAL INFORMATION:

; APPLICANT: O'Brien, John S.

; APPLICANT: Kishimoto, Yasuo

; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES

; TITLE OF INVENTION: DERIVED THEREFROM

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson and Bear

; STREET: 620 Newport Center Drive, Sixteenth Floor

; CITY: Newport Beach

; STATE: CA

; COUNTRY: USA

; ZIP: 92660

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,594A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/100,247

FILING DATE: 30-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelsen, Ned A  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-235-8550  
 TELEFAX: 619-235-0176  
 TELEX:

```
Query Match 100.0%; Score 211; DB 1; Length 80;
Best Local Similarity 100.0%; pred. No. 2.1e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5  
US-08-100-247-2  
; Sequence 2, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5

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Query Match 100.0%; Score 211; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels
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RESULT 6  
US-08-483-146A-2  
; Sequence 2, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:

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Query Match 100.0%; Score 211; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. NO. 1.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7  
US-08-232-513A-3  
; Sequence 3, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.

```

; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
; US-08-232-513A-3

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```

Query Match 100.0%; Score 211; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
 |||||||
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 349

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```

RESULT 8
US-08-484-594A-2
; Sequence 2, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/484,594A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,247  
 ; FILING DATE: 30-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israelsen, Ned A  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ;  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 523 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ;  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: N-terminal  
 ;  
 ; US-08-484-594A-2

```

Query Match 100.0%; Score 211; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFKMCSKLP 40
 |||
Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDAFKMCSKLP 349

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RESULT 9  
 US-08-100-247-1  
 ; Sequence 1, Application US/08100247  
 ; Patent No. 5571787  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'BRIEN, JOHN S.  
 ; APPLICANT: KISHIMOTO, YASUO  
 ; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
 ; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
 ; CITY: NEWPORT BEACH  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/100,247  
 ; FILING DATE: 19930730  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israelsen, Ned A.  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: O'BRIEN.002A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 22 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO



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; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: 22-MER FRAGMENT
US-08-100-247-1

Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 10
US-08-483-146A-1
; Sequence 1, Application US/08483146A
; Patent No. 5695080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-483-146A-1

Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 11

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US-08-232-513A-1
; Sequence 1, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /label- SapC
US-08-232-513A-1

Query Match 52.6%; Score 111; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

RESULT 12
US-08-484-594A-1
; Sequence 1, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,594A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,247  
; FILING DATE: 30-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-484-594A-1

Query Match 52.6%; Score 111; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 13

US-09-231-159-1  
; Sequence 1, Application US/09231159  
; Patent No. 6268347  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; CLASSIFICATION:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE: 05-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-231-159-1

Query Match 52.6%; Score 111; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 14

US-08-611-307-1  
; Sequence 1, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-611-307-1

Query Match 52.6%; Score 111; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

## RESULT 15

US-09-148-030-1  
; Sequence 1, Application US/09148030C  
; Patent No. 6458357  
; GENERAL INFORMATION:  
; APPLICANT: White, Michael T.  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Wright, David E.  
; TITLE OF INVENTION: RETRO-INVERSO NEUROTROPHIC AND ANALGESIC

; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: MYELOS.004CP1  
; CURRENT APPLICATION NUMBER: US/09/148,030C  
; CURRENT FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 08/926,015  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-148-030-1

Query Match 52.6%; Score 111; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

Search completed: June 2, 2003, 14:18:23  
Job time : 12.8077 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: June 2, 2003, 14:14:18 ; Search time 15.8974 Seconds  
(without alignments)  
254.692 Million cell updates/sec

Title: US-09-780-438C-1  
Perfect score: 211  
Sequence: 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues  
Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID               | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 211   | 100.0       | 40     | 9 US-09-780-438A-1  | Sequence 1, Appli  |
| 2          | 211   | 100.0       | 80     | 10 US-09-767-007A-3 | Sequence 3, Appli  |
| 3          | 211   | 100.0       | 80     | 10 US-09-753-126-3  | Sequence 3, Appli  |
| 4          | 211   | 100.0       | 209    | 9 US-10-043-487-340 | Sequence 340, App  |
| 5          | 211   | 100.0       | 523    | 10 US-09-767-007A-2 | Sequence 2, Appli  |
| 6          | 211   | 100.0       | 524    | 9 US-09-870-759-60  | Sequence 60, Appli |
| 7          | 211   | 100.0       | 527    | 9 US-09-870-759-61  | Sequence 61, Appli |
| 8          | 211   | 100.0       | 527    | 9 US-10-060-036-73  | Sequence 73, Appli |
| 9          | 211   | 100.0       | 592    | 10 US-09-753-126-4  | Sequence 4, Appli  |
| 10         | 201   | 95.3        | 38     | 9 US-09-780-438A-2  | Sequence 2, Appli  |
| 11         | 111   | 52.6        | 22     | 10 US-09-767-007A-1 | Sequence 1, Appli  |
| 12         | 111   | 52.6        | 22     | 10 US-09-957-143-1  | Sequence 1, Appli  |
| 13         | 96    | 45.5        | 22     | 10 US-09-767-007A-9 | Sequence 9, Appli  |
| 14         | 83    | 39.3        | 18     | 10 US-09-767-007A-5 | Sequence 5, Appli  |
| 15         | 83    | 39.3        | 18     | 10 US-09-957-143-2  | Sequence 2, Appli  |
| 16         | 75    | 35.5        | 15     | 9 US-10-293-819-2   | Sequence 2, Appli  |
| 17         | 75    | 35.5        | 15     | 10 US-09-802-617-2  | Sequence 2, Appli  |
| 18         | 75    | 35.5        | 22     | 10 US-09-767-007A-8 | Sequence 8, Appli  |
| 19         | 59    | 28.0        | 12     | 9 US-10-293-819-1   | Sequence 1, Appli  |

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| 20 | 59   | 28.0 | 12   | 10 US-09-802-617-1     | Sequence 1, Appli  |
| 21 | 59   | 28.0 | 12   | 10 US-09-957-143-3     | Sequence 3, Appli  |
| 22 | 54   | 25.6 | 172  | 10 US-09-815-153-8     | Sequence 8, Appli  |
| 23 | 51   | 24.2 | 303  | 10 US-09-864-761-36091 | Sequence 36091, A  |
| 24 | 51   | 24.2 | 997  | 9 US-09-961-403-15     | Sequence 15, Appli |
| 25 | 50   | 23.7 | 1247 | 9 US-10-032-159A-8     | Sequence 8, Appli  |
| 26 | 49.5 | 23.5 | 633  | 10 US-09-824-735-3     | Sequence 3, Appli  |
| 27 | 49.5 | 23.5 | 633  | 10 US-09-801-368-338   | Sequence 338, App  |
| 28 | 49.5 | 23.5 | 718  | 9 US-10-117-846-2      | Sequence 2, Appli  |
| 29 | 49   | 23.2 | 59   | 9 US-09-986-480-367    | Sequence 367, App  |
| 30 | 49   | 23.2 | 158  | 10 US-09-764-864-1417  | Sequence 1417, Ap  |
| 31 | 49   | 23.2 | 289  | 10 US-09-764-864-984   | Sequence 984, App  |
| 32 | 49   | 23.2 | 385  | 10 US-09-934-332-2     | Sequence 2, Appli  |
| 33 | 49   | 23.2 | 751  | 9 US-10-114-893-214    | Sequence 214, App  |
| 34 | 49   | 23.2 | 751  | 9 US-10-060-036-172    | Sequence 172, App  |
| 35 | 48.5 | 23.0 | 123  | 9 US-09-986-480-246    | Sequence 246, App  |
| 36 | 48.5 | 23.0 | 187  | 9 US-09-986-480-368    | Sequence 368, App  |
| 37 | 48.5 | 23.0 | 418  | 10 US-09-815-242-13335 | Sequence 13335, A  |
| 38 | 48   | 22.7 | 22   | 10 US-09-767-007A-6    | Sequence 6, Appli  |
| 39 | 48   | 22.7 | 179  | 9 US-10-135-807-9      | Sequence 9, Appli  |
| 40 | 48   | 22.7 | 843  | 10 US-09-815-242-5370  | Sequence 5370, Ap  |
| 41 | 48   | 22.7 | 843  | 10 US-09-815-242-12552 | Sequence 12552, A  |
| 42 | 48   | 22.7 | 843  | 10 US-09-815-242-12898 | Sequence 12898, A  |
| 43 | 47.5 | 22.5 | 62   | 10 US-09-205-658-206   | Sequence 206, App  |
| 44 | 47.5 | 22.5 | 100  | 9 US-09-820-473-4      | Sequence 4, Appli  |
| 45 | 47.5 | 22.5 | 100  | 10 US-09-820-408-4     | Sequence 4, Appli  |

ALIGNMENTS

RESULT 1  
US-09-780-438A-1  
; Sequence 1, Application US/09780438A  
; Publication No. US20030095999A1  
; GENERAL INFORMATION:  
; APPLICANT: Cincinatti Childrens Hospital Research Foundation  
; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po  
; TITLE OF INVENTION: for Application to Transmembrane Drug Delivery Systems  
; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,754  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-438A-1

|                                                                             |        |                                           |       |                                 |
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| Query Match                                                                 | 100.0% | Score 211;                                | DB 9; | Length 40;                      |
| Best Local Similarity                                                       | 100.0% | Pred. No. 7.8e-21;                        |       |                                 |
| Matches                                                                     | 40;    | Conservative                              | 0;    | Mismatches 0; Indels 0; Gaps 0; |
| Qy                                                                          | 1      | SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP | 40    |                                 |
| Db                                                                          | 1      | SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP | 40    |                                 |
| RESULT 2                                                                    |        |                                           |       |                                 |
| US-09-767-007A-3                                                            |        |                                           |       |                                 |
| ; Sequence 3, Application US/09767007A                                      |        |                                           |       |                                 |
| ; Patent No. US20020077275A1                                                |        |                                           |       |                                 |
| ; GENERAL INFORMATION:                                                      |        |                                           |       |                                 |
| ; APPLICANT: John S. O'Brien                                                |        |                                           |       |                                 |
| ; APPLICANT: Yasuo Kishimoto                                                |        |                                           |       |                                 |
| ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING                |        |                                           |       |                                 |
| ; TITLE OF INVENTION: SAPOSIN C AND NEUTROTROPIC PEPTIDES DERIVED THEREFROM |        |                                           |       |                                 |
| ; FILE REFERENCE: MYELOS.2DC1C1                                             |        |                                           |       |                                 |
| ; CURRENT APPLICATION NUMBER: US/09/767,007A                                |        |                                           |       |                                 |
| ; CURRENT FILING DATE: 2001-01-22                                           |        |                                           |       |                                 |

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; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-3

Query Match 100.0%; Score 211; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ||||||||||||||||||||||||||||||||||||||||
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 3
US-09-753-126-3
; Sequence 3, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-753-126-3

Query Match 100.0%; Score 211; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
 ||||||||||||||||||||||||||||||||||||||||
Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40

RESULT 4
US-10-043-487-340
; Sequence 340, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
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; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-340

Query Match 100.0%; Score 211; DB 9; Length 209;
Best Local Similarity 100.0%; Pred. No. 5e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
 ||||||||||||||||||||||||||||||||||||||||
Db 161 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 200

RESULT 5
US-09-767-007A-2
; Sequence 2, Application US/09767007A
; Patent No. US20020077275A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 523
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-767-007A-2

Query Match 100.0%; Score 211; DB 10; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 40
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Db 310 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSKLP 349

RESULT 6
US-09-870-759-60
; Sequence 60, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-870-759-60

Query Match 100.0%; Score 211; DB 9; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
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Db 311 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 7

US-09-870-759-61  
; Sequence 61, Application US/09870759  
; Patent No. US20020177551A1  
; GENERAL INFORMATION:  
; APPLICANT: TERMAN, David S  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
; FILE REFERENCE: 870759  
; CURRENT APPLICATION NUMBER: US/09/870,759  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 60/208,128  
; PRIOR FILING DATE: 2000-05-30  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 61  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-870-759-61

Query Match 100.0%; Score 211; DB 9; Length 527;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||  
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 353

RESULT 8

US-10-060-036-73  
; Sequence 73, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yuqiu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-73

Query Match 100.0%; Score 211; DB 9; Length 527;  
Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||  
Db 314 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 353

RESULT 9

US-09-753-126-4  
; Sequence 4, Application US/09753126  
; Patent No. US20020127219A1  
; GENERAL INFORMATION:  
; APPLICANT: OKKELS, JENS SIGURD  
; APPLICANT: JENSEN, ANNE DAM  
; APPLICANT: HALKIER, TORBEN  
; APPLICANT: JENSEN, RIKKE BOLDING  
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME  
; TITLE OF INVENTION: ACTIVATORS  
; FILE REFERENCE: 31-000600US  
; CURRENT APPLICATION NUMBER: US/09/753,126  
; CURRENT FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: PA 1999 01891  
; PRIOR FILING DATE: 1999-12-30  
; PRIOR APPLICATION NUMBER: 60/174,652  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: PA 200 00865  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/210,984  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: 60/211,124  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: PA 2000 01027  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/217,497  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
; OTHER INFORMATION: SapC-linker-GCB polypeptide  
US-09-753-126-4

Query Match 100.0%; Score 211; DB 10; Length 592;  
Best Local Similarity 100.0%; Pred. No. 1.6e-19;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
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Db 1 SDVYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40

RESULT 10

US-09-780-438A-2  
; Sequence 2, Application US/09780438A  
; Publication No. US2003009599A1  
; GENERAL INFORMATION:  
; APPLICANT: Cincinnati Childrens Hospital Research Foundation  
; TITLE OF INVENTION: Fusogenic Properties of Saposin C and Related Proteins and Po  
; TITLE OF INVENTION: for Application to Transmembrane Drug Delivery Systems  
; FILE REFERENCE: 10872/0474352  
; CURRENT APPLICATION NUMBER: US/09/780,438A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,754  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-780-438A-2

Query Match 95.3%; Score 201; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.5e-19;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 40  
|||||  
Db 1 YCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 38

## RESULT 11

US-09-767-007A-1  
; Sequence 1, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; PRIOR FILING DATE: 2001-01-22  
; PRIOR FILING DATE: 08/958,970  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-1

Query Match 52.6%; Score 111; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29  
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Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

## RESULT 12

US-09-957-143-1  
; Sequence 1, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright  
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED  
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF  
; FILE REFERENCE: MYELOS.018C1  
; CURRENT APPLICATION NUMBER: US/09/957,143  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: PCT/US00/08550  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/126,991  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-957-143-1

Query Match 52.6%; Score 111; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 4.5e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29  
|||||  
Db 1 CEFLVKEVTKLIDNNKTEKEIL 22

## RESULT 13

US-09-767-007A-9  
; Sequence 9, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-9

Query Match 45.5%; Score 96; DB 10; Length 22;  
Best Local Similarity 81.8%; Pred. No. 4.1e-06;  
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 CEFLVKEVTKLIDNNKTEKEIL 29  
|||||  
Db 1 CEFVKEVAKLIDNNRTEEEIL 22

## RESULT 14

US-09-767-007A-5  
; Sequence 5, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-5

Query Match 39.3%; Score 83; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KEVTKLIDNNKTEKEIL 29  
|||||  
Db 2 KEVTKLIDNNKTEKEIL 18

## RESULT 15

US-09-957-143-2  
; Sequence 2, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright

;  
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED  
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF  
; FILE REFERENCE: MYELOS.018C1  
; CURRENT APPLICATION NUMBER: US/09/957,143  
; CURRENT FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: PCT/US00/08550  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/126,991  
; PRIOR FILING DATE: 1999-03-30  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-09-957-143-2

Query Match 39.3%; Score 83; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.00016;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KEVTKLIDNNKTEKIL 29  
|  
Db 2 KEVTKLIDNNKTEKIL 18

Search completed: June 2, 2003, 14:17:53  
Job time : 16.8974 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 29.7179 Seconds  
(without alignments)  
170.386 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCECXEXXXKXXKXXDNNKXEXXXDXXDKXCKXX 38

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

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11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 101   | 77.1        | 80     | AA70784  | Saposin-C. Homo s  |
| 2          | 101   | 77.1        | 80     | AAW85653 | Human saposin C.   |
| 3          | 101   | 77.1        | 80     | AAU05697 | Human Saponin C, S |
| 4          | 101   | 77.1        | 523    | AAB31916 | Amino acid sequenc |
| 5          | 101   | 77.1        | 524    | AA70783  | Prosaposin. Homo   |
| 6          | 101   | 77.1        | 524    | AAW85652 | Human prosaposin N |
| 7          | 101   | 77.1        | 524    | AA58716  | Human prosaposin.  |
| 8          | 101   | 77.1        | 527    | AAB31915 | Amino acid sequenc |
| 9          | 101   | 77.1        | 592    | AAU05698 | Human glucocerebro |
| 10         | 65    | 49.6        | 25     | AAB67289 | Human saposin C.   |

|    |    |      |      |    |          |                    |
|----|----|------|------|----|----------|--------------------|
| 11 | 61 | 46.6 | 21   | 21 | AA782281 | Human saposin C 22 |
| 12 | 61 | 46.6 | 22   | 16 | AA70773  | Saposin-C neurotro |
| 13 | 61 | 46.6 | 22   | 18 | AAW30013 | Prosaposin-derived |
| 14 | 61 | 46.6 | 22   | 19 | AAW66127 | Prosaposin recepto |
| 15 | 61 | 46.6 | 22   | 20 | AAW85656 | Prosaposin recepto |
| 16 | 61 | 46.6 | 22   | 22 | AAW67305 | Peptide #5. Homo   |
| 17 | 56 | 42.7 | 22   | 18 | AAW30028 | Mutant human prosa |
| 18 | 56 | 42.7 | 22   | 19 | AAW66134 | Prosaposin derivat |
| 19 | 54 | 41.2 | 22   | 18 | AAW30018 | Bovine prosaposin- |
| 20 | 54 | 41.2 | 22   | 19 | AAW66133 | Prosaposin recepto |
| 21 | 54 | 41.2 | 22   | 20 | AAW85661 | Prosaposin recepto |
| 22 | 54 | 41.2 | 25   | 22 | AAW67293 | Bovine saposin C.  |
| 23 | 50 | 38.2 | 18   | 16 | AAW70785 | Saposin-C derived  |
| 24 | 50 | 38.2 | 18   | 18 | AAW30031 | Saposin C 12 to 29 |
| 25 | 50 | 38.2 | 18   | 19 | AAW66146 | Prosaposin recepto |
| 26 | 50 | 38.2 | 18   | 20 | AAW85655 | Prosaposin recepto |
| 27 | 50 | 38.2 | 18   | 21 | AAW82282 | Human saposin C 18 |
| 28 | 45 | 34.4 | 15   | 19 | AAW83412 | Human saposin C de |
| 29 | 45 | 34.4 | 15   | 20 | AAW99848 | Human saposin C fr |
| 30 | 45 | 34.4 | 15   | 21 | AAW83914 | Human saposin C pe |
| 31 | 45 | 34.4 | 340  | 22 | ABG22055 | Novel human diagno |
| 32 | 43 | 32.8 | 134  | 22 | ABB11113 | Human phospholipas |
| 33 | 43 | 32.8 | 554  | 23 | ABB57102 | Mouse ischaemic co |
| 34 | 43 | 32.8 | 666  | 22 | ABG12052 | Novel human diagno |
| 35 | 43 | 32.8 | 1058 | 22 | AAW80177 | Human protein SEQ  |
| 36 | 43 | 32.8 | 1216 | 22 | AAW79193 | Human protein SEQ  |
| 37 | 43 | 32.8 | 1216 | 23 | ABB08204 | Human lipid metabo |
| 38 | 42 | 32.1 | 14   | 18 | AAW30030 | Mutant human prosa |
| 39 | 42 | 32.1 | 14   | 19 | AAW66136 | Prosaposin mutant  |
| 40 | 42 | 32.1 | 359  | 22 | ABB65307 | Drosophila melanog |
| 41 | 42 | 32.1 | 2285 | 20 | AAW98149 | Bacillus subtilis  |
| 42 | 41 | 31.3 | 476  | 22 | ABB60641 | Drosophila melanog |
| 43 | 40 | 30.5 | 125  | 23 | ABP06911 | Human ORFX protein |
| 44 | 40 | 30.5 | 567  | 22 | AAW39351 | Human polypeptide  |
| 45 | 40 | 30.5 | 571  | 22 | AAW41137 | Human polypeptide  |

ALIGNMENTS

RESULT 1

AA70784

ID AAR70784 standard; Protein; 80 AA.

XX AAR70784;

XX 30-AUG-1995 (first entry)

XX Saposin-C.

KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy.

XX Homo sapiens.

XX WO9503821-A.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US08453.

XX 30-JUL-1993; 93US-0100247.

XX 21-APR-1994; 94US-0232513.

XX (OBRI/) OBRIEN J S.

XX Kishimoto Y, Obrien JS;

XX WPI; 1995-082029/11.

XX Stimulating neural cell out-growth and myelination - with

XX pro:saposin, saposin C or new neurotrophic peptide(s) from

PT

PT cytokine(s), for treating nervous system diseases  
XX  
PS Disclosure; Page 32; 50pp; English.

XX  
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuropoietic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosapoinin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.

XX  
SQ Sequence 80 AA;

Query Match 77.1%; Score 101; DB 16; Length 80;  
Best Local Similarity 55.9%; Pred. No. 7.3e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXKXXDNNKXKEXXDXDXKXCK 36  
II II II I I I I I I I I I I I I I I I I  
DB 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCSK 38

RESULT 2

AAW85653  
ID AAW85653 standard; Peptide; 80 AA.

XX  
AC AAW85653;

XX  
DT 19-JUL-1999 (first entry)

XX  
DE Human saposin C.

XX  
KW Prosapoinin; saposin; prosaptides; prosapoinin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.

XX  
OS Homo sapiens.

XX  
PN WO9912559-A1.

XX  
PD 18-MAR-1999.

XX  
PF 09-SEP-1998; 98WO-US19216.

XX  
PR 04-JUN-1998; 98US-0088129.

XX  
PR 09-SEP-1997; 97US-0058352.

XX  
PA (REGC ) UNIV CALIFORNIA.

XX  
PI O'brien JS;

XX  
DR WPI; 1999-229139/19.

XX  
PT Use of prosapoinin receptor agonist

XX  
PS Claim 7; Figure 2; 90pp; English.

XX  
CC Prosapoinin is a 70kDa glycoprotein which is proteolytically processed  
CC to generate saposins A, B, C and D, all of which are similar to each  
CC other and have a similar placement of six cysteines, a glycosylation

CC site and conserved proline residues. Prosapoinin, saposin C and  
CC prosapoinin derived peptides (prosaptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ishchaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosapoinin receptor agonists (PRAs)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAs block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC activation of JNK by TNF alpha is another well known mechanism for  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is  
CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. Saposin C acts as a prosapoinin receptor agonist.

XX  
SQ Sequence 80 AA;

Query Match 77.1%; Score 101; DB 20; Length 80;  
Best Local Similarity 55.9%; Pred. No. 7.3e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXKXXDNNKXKEXXDXDXKXCK 36  
II II II I I I I I I I I I I I I I I I I  
DB 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCSK 38

RESULT 3

AAU05697  
ID AAU05697 standard; Protein; 80 AA.

XX  
AC AAU05697;

XX  
DT 24-OCT-2001 (first entry)

XX  
DE Human Saponin C, SapC.

XX  
KW Human; glucocerebrosidase; GCB; lysosomal storage disease;

KW Gaucher's disease; Fabry's disease; Farber's disease;

KW G\_m\_1 gangliosidosis; Tay-Sachs's disease; Niemann-Pick disease;

KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;

KW Scheie syndrome; Saponin C; SapC.

XX  
OS Homo sapiens.

XX  
PN WO200149830-A2.

XX  
PD 12-JUL-2001.

XX  
PF 29-DEC-2000; 2000WO-DK00743.

XX  
PR 30-DEC-1999; 99DK-0001891.

XX  
PR 02-JUN-2000; 2000DK-0000865.

XX  
PR 02-JUN-2000; 2000DK-0000866.

XX  
PR 30-JUN-2000; 2000DK-0001027.

XX  
PA (MAXY-) MAXYGEN APS.

XX  
PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;



DR WPI; 2001-465259/50.  
XX Improved lysosomal enzymes and lysosomal enzyme activators useful for  
PT treating Gaucher's disease -  
XX  
PS Example 5; Page 96; 97pp; English.  
XX  
CC The sequence represents human Saposin C (SapC), an essential  
CC co-factor for the lysosomal enzyme glucocerebrosidase,  
CC GCB. GCB is the enzyme involved in Gaucher's disease, a lysosomal  
CC storage disease. The invention relates to introducing new glycosylation  
CC sites into lysosomal enzymes/activators like GCB to improve their  
CC bioactivity. The novel polypeptides are used for the prevention and  
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,  
CC G\_m1 gangliosidosis, Tay-Sachs's disease, Niemann-Pick disease, Shindler  
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie  
CC syndromes.  
XX  
SQ Sequence 80 AA;  
Query Match 77.1%; Score 101; DB 22; Length 80;  
Best Local Similarity 55.9%; Pred. No. 7.3e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 3 CEXCEXXXKEXKXNDNNKXKEXKXDXDXKXCXK 36  
DB 5 CEVCEFLVKEVTKLIDNNKTEKELDAFDKMCCK 38  
RESULT 4  
AAB31916  
ID AAB31916 standard; Protein; 523 AA.  
XX  
AC AAB31916;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Amino acid sequence of a human protein.  
XX  
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200105422-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 17-JUL-2000; 2000WO-FR02057.  
XX  
PR 15-JUL-1999; 99FR-0009372.  
XX  
PA (INMR ) BIOMERIEUX STELHYS.  
XX  
PI Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
XX WPI; 2001-159475/16.  
XX  
XX Detecting, preventing and treating degenerative, neurological and  
PT autoimmune diseases, particularly multiple sclerosis, using specified  
PT polypeptides or related nucleic acid or ligand -  
XX  
PS Claim 1; Page 174-175; 209pp; French.  
XX  
CC The present sequence represents a human protein, which is used in the  
CC method of the invention. The specification describes a method which uses  
CC at least one polypeptide or polynucleotide sequence belonging to the  
CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
CC families. The method is used for detecting, preventing or treating a

CC degenerative, neurological and/or auto-immune disease. The  
CC polynucleotides and polypeptides are used for diagnosis, prognosis,  
CC prevention and treatment of multiple sclerosis (in its various forms  
CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
CC polyarthritis and lupus erythematosus, including use as vaccines and  
CC in gene therapy (expression of sense or antisense sequences). They can  
CC also be used to assess efficacy of potential therapeutic agents,  
CC particularly compounds that reduce or inhibit toxicity towards glial  
CC cells.  
XX  
SQ Sequence 523 AA;  
Query Match 77.1%; Score 101; DB 22; Length 523;  
Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 3 CEXCEXXXKEXKXNDNNKXKEXKXDXDXKXCXK 36  
DB 314 CEVCEFLVKEVTKLIDNNKTEKELDAFDKMCCK 347  
RESULT 5  
AAR70783  
ID AAR70783 standard; Protein; 524 AA.  
XX  
AC AAR70783;  
XX  
DT 30-AUG-1995 (first entry)  
XX  
DE Prosaposin.  
XX  
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy; prosaposin.  
XX  
OS Homo sapiens.  
XX  
PN WO9503821-A.  
XX  
PD 09-FEB-1995.  
XX  
PF 28-JUL-1994; 94WO-US08453.  
XX  
PR 30-JUL-1993; 93US-0100247.  
PR 21-APR-1994; 94US-0232513.  
XX  
PA (OBRI/) OBRIEN J S.  
XX  
PI Kishimoto Y, O'Brien JS;  
XX WPI; 1995-082029/11.  
DR N-PSDB; AAQ85355.  
XX  
PT Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases  
XX  
PS Disclosure; Page 30-32; 50pp; English.  
XX  
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuroepithelial cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosaposin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.  
XX  
SQ Sequence 524 AA;  
Query Match 77.1%; Score 101; DB 16; Length 524;



CC has potent antiangiogenic and antitumour activity, and also has  
CC antiproliferative and antimigratory activity against endothelial  
CC cells. This activity is conserved in cryptic polypeptides as small  
CC as 5 amino acids (see AAY58684-715), which can be synthetically  
CC prepared and used in vitro or in vivo for the treatment of  
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma  
CC (claimed). The polypeptides can also be used in conjunction with  
CC cytotoxic moieties to selectively kill certain cell types, e.g. for  
CC treatment of cancer, angiofibroma, neovascular glaucoma,  
CC arteriovenous malformation, nonunion fracture, arthritis and other  
CC connective tissue disorders, Osler-Weber syndrome, atherosclerotic  
CC plaque, psoriasis, corneal graft neovascularization, pyogenic  
CC granuloma, retrolental fibroplasia, diabetic retinopathy,  
CC scleroderma, haemangioma, trachoma, vascular adhesions and  
CC hypertrophic scars.

XX Sequence 524 AA;  
SQ

Query Match 77.1%; Score 101; DB 21; Length 524;  
Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXXXNNKXEXXDXDXKXCXK 36  
II II I I I I I I I I I I I I I I I I I  
Db 315 CEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSK 348

RESULT 8  
AAB31915  
ID AAB31915 standard; Protein; 527 AA.  
XX  
AC AAB31915;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Amino acid sequence of a human protein.  
XX  
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200105422-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 17-JUL-2000; 2000WO-FR02057.  
XX  
PR 15-JUL-1999; 99FR-0009372.  
XX  
PA (INMR ) BIOMERIEUX STELHYS.  
XX  
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
XX  
DR WPI; 2001-159475/16.  
XX  
PT Detecting, preventing and treating degenerative, neurological and  
PT autoimmune diseases, particularly multiple sclerosis, using specified  
PT polypeptides or related nucleic acid or ligand -  
XX  
PS Claim 1; Page 172-173; 209pp; French.  
XX  
CC The present sequence represents a human protein, which is used in the  
CC method of the invention. The specification describes a method which uses  
CC at least one polypeptide or polynucleotide sequence belonging to the  
CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
CC families. The method is used for detecting, preventing or treating a  
CC degenerative, neurological and/or auto-immune disease. The  
CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms  
CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
CC polyarthritis and lupus erythematosus, including use as vaccines and  
CC in gene therapy (expression of sense or antisense sequences). They can  
CC also be used to assess efficacy of potential therapeutic agents,  
CC particularly compounds that reduce or inhibit toxicity towards glial  
CC cells.

XX  
SQ Sequence 527 AA;  
Query Match 77.1%; Score 101; DB 22; Length 527;  
Best Local Similarity 55.9%; Pred. No. 4.6e-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXXXNNKXEXXDXDXKXCXK 36  
II II I I I I I I I I I I I I I I I I I  
Db 318 CEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSK 351

RESULT 9  
AAU05698  
ID AAU05698 standard; Protein; 592 AA.  
XX  
AC AAU05698;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human glucocerebrosidase, GCB-Saponin C, SapC, fusion protein.  
XX  
KW Human; glucocerebrosidase; GCB; lysosomal storage disease;  
KW Gaucher's disease; Fabry's disease; Farber's disease;  
KW G\_m\_1 gangliosidosis; Tay-Sach's disease; Niemann-Pick disease;  
KW Shindler disease; Hunter syndrome; Sly syndrome; Hurler syndrome;  
KW Scheie syndrome; fusion protein; Saponin C; SapC.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Protein 1..80  
FT Peptide /label= SapC  
FT Protein 81..95  
FT Modified-site /label= Linker\_peptide  
FT Modified-site 96..592  
FT Modified-site /label= GCB  
FT Modified-site 114  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 154  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 241  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 365  
FT Modified-site /note= "N-glycosylated"

XX  
PN WO200149830-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 29-DEC-2000; 2000WO-DK00743.  
XX  
PR 30-DEC-1999; 99DK-0001891.  
PR 02-JUN-2000; 2000DK-0000865.  
PR -02-JUN-2000; 2000DK-0000866.  
PR 30-JUN-2000; 2000DK-0001027.  
XX  
PA (MAXY-) MAXYGEN APS.  
XX  
PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;  
XX WPI; 2001-465259/50.  
XX  
PT Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -

XX Example 5; Page 96-97; 97pp; English.

PS

CC The sequence is a fusion protein of human lysosomal enzyme

CC glucocerebrosidase, GCB and its co-factor, Saponin C, SapC.

CC GCB is the enzyme involved in Gaucher's disease, a lysosomal

CC storage disease. The invention relates to introducing new glycosylation

CC sites into lysosomal enzymes/activators like GCB to improve their

CC bioactivity. The novel polypeptides are used for the prevention and

CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,

CC G\_m\_1 gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler

CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie

CC syndromes.

XX

SQ Sequence 592 AA;

Query Match 77.1%; Score 101; DB 22; Length 592;

Best Local Similarity 55.9%; Pred. No. 5.2e-09;

Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXXXNNKXEXXDXDXKXK 36

DB 5 CEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCK 38

RESULT 10

AAB67289

ID AAB67289 standard; Peptide; 25 AA.

XX

AC AAB67289;

XX

DT 20-APR-2001 (first entry)

XX

DE Human saposin C.

XX

KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

XX

OS Homo sapiens.

XX

PN EP1072609-A2.

XX

PD 31-JAN-2001.

XX

PF 30-JUN-2000; 2000EP-0305504.

XX

PR 30-JUN-1999; 99JP-0185155.

XX

PA (SAKA/) SAKANAKA M.

PA (TANA/) TANAKA J.

PA (SATO/) SATO K.

XX

PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;

XX

DR WPI; 2001-204263/21.

XX

PT Use of prosaposin-related peptides or derivatives as cytoprotective

PT agents, for suppressing apoptosis or apoptosis-like cell death -

XX

PS Disclosure; Page 12; 41pp; English.

XX

CC The present invention relates to use of a prosaposin-related peptide

CC or derivative, in the production of a medicament for use in

CC preventing or delaying cell death, or in promoting the expression

CC of cell death supporting gene product Bcl-XL. The invention is

CC useful for preventing the death of cells e.g. brain cells,

CC neurons and cardiac muscle cells, in vitro or ex vivo.

XX

SQ Sequence 25 AA;

Query Match 49.6%; Score 65; DB 22; Length 25;

Best Local Similarity 56.5%; Pred. No. 0.00029;

Matches 13; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXXXNNKXEXXDX 28

DB 1 CEFLVKEVTKLIDNNKTEKEILD 23

RESULT 11

AAY82281

ID AAY82281 standard; peptide; 21 AA.

XX

AC AAY82281;

XX

DT 16-JUN-2000 (first entry)

XX

DE Human saposin C 22-mer peptide SEQ ID NO:1.

XX

KW Cyclic; prosaposin; neurotrophic; analgesic; neural growth; cell death;

KW myelination; neurodegenerative disorder; neuropathic pain; vasotropic;

KW saposin C; neuroprotective; vulnary; analgesic; antiparkinsonian;

KW ophthalmological; demyelination; multiple sclerosis; ischaemic injury;

KW traumatic injury; Parkinson's disease; retinal neuropathy;

KW ocular neurodegeneration.

XX

OS Homo sapiens.

XX

PN WO200012553-A1.

XX

PD 09-MAR-2000.

XX

PF 20-AUG-1999; 99WO-US19378.

XX

PR 28-AUG-1998; 98US-0098359.

XX

PA (MYEL-) MYELOS CORP.

XX

PI Wright DE, O'Brien JS;

XX

DR WPI; 2000-256591/22.

XX

PT New peptide derived from saposin C, useful to treat demyelination,

PT neural degeneration and neurological pain, is circular and thus

PT resistant to proteolytic degradation -

XX

PS Disclosure; Page 2; 30pp; English.

XX

CC The present invention describes a cyclic peptide of about 11-25 amino

CC acids containing an analogue of the 11-mer active region of saposin C.

CC The cyclic peptide has neuroprotective, vasotropic, vulnary,

CC analgesic, antiparkinsonian and ophthalmological activities. It

CC stimulates choline acetyltransferase activity. The peptide is used to

CC induce myelination or inhibit demyelination in a mammal, especially a

CC human, where demyelination is due to multiple sclerosis, ischaemic

CC injury or traumatic injury, to inhibit neural degeneration or promote

CC neurite outgrowth in neural tissue and treat neuropathic pain. The

CC peptide may also be useful to treat Parkinson's disease, retinal

CC neuropathy, and ocular neurodegeneration leading to vision loss in the

CC elderly. The peptide can be used in research to study the effects of

CC neurotrophic factors and myelin facilitating materials, and as

CC components of cell growth media for facilitating and maintaining neural

CC cells in vitro. The invention provides circular prosaposin

CC peptidomimetics which are more resistant to proteolytic degradation and

CC better able to cross the blood brain barrier than prior art linear

CC peptides. The present sequence represents a human saposin C 22-mer

CC peptide given in the disclosure of the present invention.

XX

SQ Sequence 21 AA;

Query Match 46.6%; Score 61; DB 21; Length 21;

Best Local Similarity 60.0%; Pred. No. 0.0011;

Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXXXNNKXEXKE 25

Db 1 CEFLVKEVTKLIDNNKTEKE 20

RESULT 12  
AAR70773

ID AAR70773 standard; peptide; 22 AA.  
XX  
AC AAR70773;  
XX  
DT 30-AUG-1995 (first entry)  
XX  
DE Saposin-C neurotrophic peptide.  
XX  
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy.  
XX  
OS Homo sapiens.  
XX  
PN WO9503821-A.  
XX  
PD 09-FEB-1995.  
XX  
PF 28-JUL-1994; 94WO-US08453.  
XX  
PR 30-JUL-1993; 93US-0100247.  
PR 21-APR-1994; 94US-0232513.  
XX  
PA (OBRI/) OBRIEN J S.  
PI Kishimoto Y, Obrien JS;  
XX  
DR WPI; 1995-082029/11.  
XX  
PT Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases  
XX  
PS Disclosure; Page 30; 50pp; English.  
XX

CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuroepithelial cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosapinin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.  
XX  
SQ Sequence 22 AA;

Query Match 46.6%; Score 61; DB 16; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXEKE 25  
|| || | ||| |||  
Db 1 CEFLVKEVTKLIDNNKTEKE 20

RESULT 13  
AAW30013

ID AAW30013 standard; peptide; 22 AA.  
XX  
AC AAW30013;  
XX  
DT 14-APR-1998 (first entry)  
XX  
DE Prosapinin-derived peptide 22-mer.  
XX  
KW Human; prosapinin; neural disorder; demyelination disorder;  
KW neural cell death; inhibition; myelination; neurite outgrowth;

KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;  
KW polyneuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus.  
XX  
OS Homo sapiens.  
XX  
PN WO9732895-A1.  
XX  
PD 12-SEP-1997.  
XX  
PF 05-MAR-1997; 97WO-US04143.  
XX  
PR 05-MAR-1996; 96US-0611307.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI O'Brien JS;  
XX  
DR WPI; 1997-470538/43.  
XX  
PT Prosapinin-derived peptide - useful for therapy of neural or  
PT demyelination disorders in neural tissue  
XX  
PS Claim 9; Page 52; 69pp; English.  
XX

CC The present sequence represents a prosapinin-derived peptide. A method  
CC has been developed of alleviating or preventing neuropathic pain in a  
CC subject, comprising administering an effective amount of an active  
CC fragment of prosapinin to the subject. The prosapinin-derived peptide  
CC is useful for therapy of neural or demyelination disorders in neural  
CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural  
CC cell death, promote myelination or inhibit demyelination. The method  
CC is used to alleviate neuropathic pain resulting from a peripheral nerve  
CC disorder, such as neuroma, nerve compression, crush or stretch and  
CC incomplete nerve transection, mononeuropathy or polyneuropathy.  
CC Alternatively the neuropathic pain results from a disorder of the  
CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.  
XX  
SQ Sequence 22 AA;

Query Match 46.6%; Score 61; DB 18; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXEKE 25  
|| || | ||| |||  
Db 1 CEFLVKEVTKLIDNNKTEKE 20

RESULT 14  
AAW66127

ID AAW66127 standard; peptide; 22 AA.  
XX  
AC AAW66127;  
XX  
DT 17-NOV-1998 (first entry)  
XX  
DE Prosapinin receptor agonist #1.  
XX  
KW prosapinin; receptor agonist; neuropathic pain; neurite outgrowth;  
KW neural cell death; nerve disorder; side effect.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9839357-A1.  
XX  
PD 11-SEP-1998.  
XX  
PF 11-SEP-1997; 97WO-US16062.  
XX  
PR 05-MAR-1997; 97WO-US04143.  
XX  
PA (REGC ) UNIV CALIFORNIA.

XX O'Brien JS;  
PI WPI; 1998-495790/42.  
XX N-PSDB; AAV07664.  
DR Use of prosaposin receptor agonists - for alleviating neuropathic  
XX pain, inhibiting sensory or motor neuropathy, or inhibiting neural  
PT cell death  
PT Claim 3; Page 2; 67pp; English.  
XX  
PS The invention relates to prosaposin receptor agonists. Also claimed  
XX are: (1) methods for alleviating neuropathic pain or inhibiting the  
CC onset of neuropathic pain, comprising administering a prosaposin receptor  
CC agonist; (2) inhibiting sensory or motor neuropathy, comprising  
CC contacting neuronal cells with a composition comprising a prosaposin  
CC receptor agonist; (3) methods for stimulating neurite outgrowth,  
CC inhibiting neural cell death, promoting myelination, or inhibiting  
CC demyelination comprising contacting neuronal cells with a composition  
CC comprising a prosaposin receptor agonist which has 14-50 amino acids and  
CC comprises the sequence of a prosaposin derived protein. The processes  
CC may be used for treatment of neuropathic pain resulting from peripheral  
CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve  
CC stretch, incomplete nerve transection, mononeuropathy or polyneuropathy)  
CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the  
CC thalamus or the cortex. The receptor agonists do not cause undesirable  
CC side effects. The present sequence represents a specifically claimed  
CC prosaposin receptor agonist.  
XX  
SQ Sequence 22 AA;  
  
Query Match 46.6%; Score 61; DB 19; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 6 CEXXXKEXXXDNNKXEKE 25  
II II I III III  
Db 1 CEFLVKEVTKLIDNNKTEKE 20  
  
RESULT 15  
AAW85656  
ID AAW85656 standard; Peptide; 22 AA.  
XX AAW85656;  
AC  
XX 19-JUL-1999 (first entry)  
DT Prosaposin receptor agonist.  
XX  
DE Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
XX PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
XX WO9912559-A1.  
PN  
XX  
PD 18-MAR-1999.  
XX  
XX 09-SEP-1998; 98WO-US19216.  
PF  
XX

PR 04-JUN-1998; 98US-0088129.  
PR 09-SEP-1997; 97US-0058352.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX O'Brien JS;  
PI  
XX WPI; 1999-229139/19.  
DR Use of prosaposin receptor agonist  
XX  
PT Claim 7; Page 66; 90pp; English.  
XX  
PS Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
CC to generate saposins A, B, C and D, all of which are similar to each  
CC other and have a similar placement of six cysteines, a glycosylation  
CC site and conserved proline residues. Prosaposin, saposin C and  
CC prosaposin derived peptides (prosaptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ishchaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosaposin receptor agonists (PRAs)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAs block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC activation of JNK by TNF alpha is another well known mechanism for  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is  
CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This peptide corresponds to amino acids 8 to 29 of  
CC human saposin C (See AAW85653) and acts as a prosaposin receptor  
CC agonist.  
XX  
SQ Sequence 22 AA;  
  
Query Match 46.6%; Score 61; DB 20; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 6 CEXXXKEXXXDNNKXEKE 25  
II II I III III  
Db 1 CEFLVKEVTKLIDNNKTEKE 20  
  
Search completed: June 2, 2003, 14:15:45  
Job time : 30.7179 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:14 ; Search time 13.641 Seconds  
(without alignments)  
267.803 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXXKXXKXXKXXDNNKXKEXXDXDXKXXKXX 38

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues 283224  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description        |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 101   | 77.1        | 527    | 1  | SAHUP  | saposin precursor  |
| 2          | 84    | 64.1        | 80     | 2  | S21770 | saposin-C - bovine |
| 3          | 61    | 46.6        | 81     | 2  | A32026 | glucosylceramide b |
| 4          | 46    | 35.1        | 554    | 1  | A28716 | saposin precursor  |
| 5          | 43    | 32.8        | 557    | 1  | JH0604 | saposin precursor  |
| 6          | 43    | 32.8        | 913    | 2  | T46339 | hypothetical prote |
| 7          | 43    | 32.8        | 1216   | 2  | A28822 | 1-phosphatidylinos |
| 8          | 43    | 32.8        | 1216   | 2  | A28821 | 1-phosphatidylinos |
| 9          | 42    | 32.1        | 314    | 2  | T15674 | hypothetical prote |
| 10         | 42    | 32.1        | 483    | 2  | S41853 | centromere/microtu |
| 11         | 42    | 32.1        | 965    | 2  | T00207 | p109 protein - sil |
| 12         | 42    | 32.1        | 2285   | 2  | T12796 | probable transglyc |
| 13         | 41.5  | 31.7        | 473    | 2  | F70031 | cell wall-binding  |
| 14         | 41    | 31.3        | 419    | 2  | T18450 | hypothetical prote |
| 15         | 40    | 30.5        | 191    | 1  | H69472 | iron-dependent rep |
| 16         | 40    | 30.5        | 301    | 2  | T33068 | hypothetical prote |
| 17         | 40    | 30.5        | 347    | 2  | T39392 | hypothetical prote |
| 18         | 40    | 30.5        | 519    | 2  | S54014 | hypothetical prote |
| 19         | 40    | 30.5        | 570    | 2  | T08778 | hypothetical prote |
| 20         | 40    | 30.5        | 731    | 2  | B86132 | hypothetical prote |
| 21         | 40    | 30.5        | 735    | 2  | G91290 | hypothetical prote |
| 22         | 39.5  | 30.2        | 165    | 2  | T52114 | probable transcrip |
| 23         | 39.5  | 30.2        | 263    | 2  | G87721 | protein ZC123.3 [i |
| 24         | 39.5  | 30.2        | 1377   | 2  | T19214 | UDP-glucose-glycop |
| 25         | 39    | 29.8        | 189    | 2  | S44639 | hypothetical prote |
| 26         | 39    | 29.8        | 210    | 2  | T28771 | hypothetical prote |
| 27         | 39    | 29.8        | 211    | 2  | T25911 | hypothetical prote |
| 28         | 39    | 29.8        | 315    | 2  | T16874 | hypothetical prote |
| 29         | 39    | 29.8        | 572    | 2  | T20764 | hypothetical prote |

30 39 29.8 641 2 F71810 type III DNA modif  
31 39 29.8 1173 1 A53430 1-phosphatidylinos  
32 39 29.8 3498 2 T22330 hypothetical prote  
33 38.5 29.4 330 2 B71625 rifin PFB0040C - m  
34 38 29.0 183 2 F84636 hypothetical prote  
35 38 29.0 568 2 F71614 chromatinic RING f  
36 38 29.0 614 2 B71884 hypothetical prote  
37 38 29.0 614 2 D64630 hypothetical prote  
38 38 29.0 921 2 T19694 hypothetical prote  
39 38 29.0 1451 2 A36468 SPT6 protein - yea  
40 38 29.0 2706 2 T28155 variant-specific s  
41 37.5 28.6 264 2 T14261 dnaK-type molecula  
42 37.5 28.6 489 1 D64311 fumarate reductase  
43 37.5 28.6 668 2 S21880 dnaK-type molecula  
44 37.5 28.6 1390 2 S51364 sperm tail-specifi  
45 37 28.2 139 2 A24154 85K major surface

ALIGNMENTS

RESULT 1

SAHUP  
saposin precursor [validated] - human  
N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon  
ein (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein  
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1992 #sequence\_revision 17-Nov-1995 #text\_change 08-Dec-2000  
C:Accession: JX0061; A57368; A42003; B42003; C42003; D42003; A30367; S34740; S36140;  
0226; I37265; I37264  
R:Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.  
J. Biochem. 105, 152-154, 1989  
A:Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-gluc  
A:Reference number: JX0061; MUID:89255151; PMID:2498298  
A:Accession: JX0061  
A:Molecule type: mRNA  
A:Residues: 1-527 <NAK>  
A:Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064  
A:Note: alternative splice form 1  
A:Accession: A57368  
A:Molecule type: mRNA  
A:Residues: 1-259,263-527 <NA2>  
A:Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756  
A:Note: alternative splice form 2  
R:Rorman, E.G.; Scheinker, V.; Grabowski, G.A.  
Genomics 13, 312-318, 1992  
A:Title: Structure and evolution of the human prosaposin chromosomal gene.  
A:Reference number: A42003; MUID:92307663; PMID:1612590  
A:Accession: A42003  
A:Molecule type: DNA  
A:Residues: 50-140 <ROR>  
A:Cross-references: GB:M86181  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)  
A:Accession: B42003  
A:Molecule type: DNA  
A:Residues: 185-259,263-276 <RO2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)  
A:Accession: C42003  
A:Molecule type: DNA  
A:Residues: 305-393 <RO3>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence  
A:Accession: D42003  
A:Molecule type: DNA  
A:Residues: 399-487 <RO4>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence  
R:Rorman, E.G.; Grabowski, G.A.  
Genomics 5, 486-492, 1989  
A:Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sp  
A:Reference number: A30367; MUID:90129043; PMID:2515150  
A:Accession: A30367  
A:Molecule type: mRNA  
A:Residues: 1-259,263-527 <RO5>

A;Cross-references: GB:J03077; NID:g183230; PIDN:AAA52560.1; PID:g183231  
A;Note: alternative splice form 2  
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993  
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor  
A;Reference number: S34740; MUID:93311991; PMID:833276  
A;Accession: S34740  
A;Molecule type: protein  
A;Residues: 17-24;165-172;180-189;301-305 <HIR>  
R;Tyynelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993  
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.  
A;Reference number: S36140; MUID:93380576; PMID:8370464  
A;Accession: S36140  
A;Molecule type: protein  
A;Residues: 'XX',62,'X',64-65,'X',67-79,'X',81-84 <TYV>  
A;Note: saposin A  
A;Accession: S36141  
A;Molecule type: protein  
A;Residues: 'XXX',413-414,'X',416-428,'X',430-434 <TY2>  
A;Note: saposin D  
R;Holtzschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7556-7560, 1991  
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and  
A;Reference number: S36988; MUID:91210267; PMID:2019586  
A;Accession: S36988  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-257 <HO>  
A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-259,263-527 <HO2>  
A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-259,261-527 <HO3>  
A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative splicing  
R;Kondoh, K.; Hinenio, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991  
A;Title: Isolation and characterization of prosaposin from human milk.  
A;Reference number: PS0330; MUID:92068206; PMID:1958198  
A;Accession: PS0330  
A;Molecule type: protein  
A;Residues: 17-24,'X',26 <KON>  
A;Experimental source: milk  
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990  
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation  
A;Reference number: A35985; MUID:90207231; PMID:2320574  
A;Accession: A35985  
A;Molecule type: mRNA  
A;Residues: 213-221 <KRE>  
A;Cross-references: GB:M32221  
A;Accession: B35985  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-259,263-527 <KR2>  
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762  
A;Experimental source: lymphoblast  
A;Accession: C35985  
A;Molecule type: mRNA  
A;Residues: 213-216,'I',218-221 <KR3>  
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; the  
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990  
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein  
A;Reference number: S13195; MUID:91006165; PMID:2209618  
A;Accession: S13196  
A;Molecule type: protein  
A;Residues: 195-259,263-277 <FUE>  
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989  
A;Title: Saposin A: second cerebroside activator protein.  
A;Reference number: A32784; MUID:89240739; PMID:2717620  
A;Accession: A32784  
A;Molecule type: protein  
A;Residues: 60-84;86-107;109-119;125-134 <MOR>  
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988  
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene  
A;Reference number: A41240; MUID:88321660; PMID:2842863  
A;Accession: A41240  
A;Molecule type: mRNA  
A;Residues: 'GSSR',18-259,263-299,'D',301-302,'D',304-527 <OAB>  
A;Cross-references: GB:J03086  
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987  
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein  
A;Reference number: S02289; MUID:88068647; PMID:2825202  
A;Accession: S02289  
A;Status: significant sequence differences  
A;Molecule type: mRNA  
A;Cross-references: EMBL:J03015  
A;Note: this sequence corrected by A41240  
A;Note: part of this sequence, including the amino end of the mature protein, was determined  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988  
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein  
A;Reference number: S02028; MUID:89207118; PMID:3242555  
A;Accession: S02028  
A;Molecule type: protein  
A;Residues: 195-259,263-276 <KLE>  
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988  
A;Title: The precursor of sulfatide activator protein is processed to three different  
A;Reference number: S00813; MUID:89000190; PMID:3048308  
A;Accession: S00813  
A;Molecule type: protein  
A;Residues: 410-487 <FU2>  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987  
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurring  
A;Reference number: S00226; MUID:88163077; PMID:3442600  
A;Accession: S00226  
A;Molecule type: protein  
A;Residues: 314-393 <KL2>  
R;Vaccaro, A.M.; Salvioli, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia J. Biol. Chem. 270, 9953-9960, 1995  
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bonds  
A;Reference number: A57297; MUID:95247790; PMID:7730378  
A;Contents: annotation; disulfide bonds; glycosylation  
R;Holtzschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991  
A;Title: The organization of the gene for the human cerebroside sulfate activator protein  
A;Reference number: I37264; MUID:91192146; PMID:2013321  
A;Accession: I37265  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 59-125 <RES>  
A;Cross-references: EMBL:X57107; NID:g30234; PIDN:CAA40391.1; PID:g30235  
A;Accession: I37264  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 307-516 <RE2>  
A;Cross-references: EMBL:X57108; NID:g30232; PIDN:CAA40392.1; PID:g1565257  
A;Note: sequence revised relative to PID:g30233 (corrected coding region)  
C;Genetics.

A;Gene: GDB:PSAP; GLBA  
A;Cross-references: GDB:120366; OMIM:176801  
A;Map position: 10q22.1-10q22.1  
A;Introns: 83/3; 338/3; 401/1; 453/3; 480/3  
A;Note: defects in this gene may cause variant Tay-Sachs disease, variant Tay-Sachs disease  
A;Note: list of introns is incomplete

```
Query Match 77.1%; Score 101; DB 1; Length 527;
Best Local Similarity 55.9%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

|    |     |                                |     |
|----|-----|--------------------------------|-----|
| Qy | 3   | CECEXXXXXXDNNKXEXDXDXKXCK      | 36  |
|    |     |                                |     |
| Db | 318 | CEVCEFLVXETKLDNNKTEKEILDAFKMCK | 351 |

```

RESULT 2
S21770
saposin-C - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S21770
R:Sano, A.; Mizuno, T.; Kondoh, K.; Hinenno, T.; Ueno, S.; Kakimoto, Y.; Morita, N.
Biochim. Biophys. Acta 1120, 75-80, 1992
A:Title: Saposin-C from bovine spleen; complete amino acid sequence and relation between
A:Reference number: S21770; MUID:92207994; PMID:1554743
A:Accession: S21770
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-80 <SAN>
C:Superfamily: saposin; saposin repeat homology

```

```
Query Match 64.1%; Score 84; DB 2; Length 80;
Best Local Similarity 44.1%; Pred. NO. 3.8e-07;
Matches 15; Conservative 3; Mismatches 16; Indels 0; Gaps 0;
```

|    |   |                                  |    |
|----|---|----------------------------------|----|
| QY | 3 | CEXEXXXKEXXXXXNNKXEKEEXDXXDKXCXK | 36 |
|    |   | :                                |    |
| Db | 5 | CQCFVVKVEKAKLIDNNTTEEEIHALDKVCCK | 38 |

RESULT 3  
A32026  
glucosylceramide beta-glucosidase activator protein SAP-2 - guinea pig  
C/Species: *Cavia porcellus* (guinea pig)  
C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 17-May-1996  
C/Accession: A32026  
R/Sano, A.; Radin, N.S.; Johnson, L.L.; Tarr, G.E.  
J. Biol. Chem. 263, 19597-19601, 1988  
A/Title: The activator protein for glucosylceramide beta-glucosidase from guinea pig liver  
A/Reference number: A32026; MUID:89066787; PMID:3198642  
A/Accession: A32026  
A/Molecule type: protein  
A/Residues: 1-81 <SAN>  
C/Superfamily: saposin; saposin repeat homology  
F;1-81/Domain: saposin repeat homology <SAP>

```

Query Match 46.6%; Score 61; DB 2; Length 81;
Best Local Similarity 31.2%; Pred. NO. 0.0026;
Matches 10; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

```

|    |   |     |     |     |      |      |      |     |     |      |         |    |
|----|---|-----|-----|-----|------|------|------|-----|-----|------|---------|----|
| Qy | 3 | CEC | EXX | KEX | XXXX | NN   | KEX  | XXD | XXD | KXC  | 34      |    |
|    |   | 1:  | 1:  | 1:  | :    | 111: | 1:   | :   | :   | 1    |         |    |
| Dd | 5 | CKA | CEY | VV  | KK   | VM   | ELID | NN  | RT  | EKII | HALDSVC | 36 |

RESULT 4  
A28716  
saposin precursor - rat  
N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component ein (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfata N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A28716  
R;Collard, M.W.; Sylvestre, S.R.; Tsuruta, J.K.; Griswold, M.D.  
Biochemistry 27, 4557-4564, 1988  
A;Title: Biosynthesis and molecular cloning of sulfated glycoprotein 1 secreted by rat  
A;Reference number: A28716; MUID:89000647; PMID:3048385  
A;Accession: A28716  
A;Molecule type: mRNA  
A;Residues: 1-554 <COL>  
A;Cross-references: GB:M19936; NID:g206904; PIDN:AAA42136.1; PID:g206905  
A;Note: parts of this sequence, including the amino end of the mature protein, were d  
C;Function:

A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them  
A;Pathway: sphingolipid catabolism  
A;Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-glucosidase  
A;Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by arylsulfatase  
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiesterase  
C;Superfamily: saposin; saposin repeat homology  
C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome;  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-554/Product: prosaposin #status predicted <PRO>  
F;55-148/Domain: saposin repeat homology <SAP1>  
F;60-143/Product: saposin A #status predicted <SAPA>  
F;189-280/Domain: saposin repeat homology <SAP2>  
F;194-273/Product: saposin B #status predicted <SAB1>  
F;306-397/Domain: saposin repeat homology <SAP3>  
F;310-389/Product: saposin C #status predicted <SAPC>  
F;431-522/Domain: saposin repeat homology <SAP4>  
F;437-514/Product: saposin D #status predicted <SAPD>  
F;63-138,66-132,94-106,439-512,442-506,470-481/Disulfide bonds: #status predicted  
F;80,214,331,456/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;197-270,200-264,229-240,314-387,317-381,345-356/Disulfide bonds: #status predicted

Query Match 35.1%; Score 46; DB 1; Length 554;  
Best Local Similarity 25.0%; pred. NO. 3.9;  
Matches 8; Conservative 5; Mismatches 19; Indels

|    |    |                                 |    |
|----|----|---------------------------------|----|
| Qy | 3  | CEXCEXXXKEXXXXXNNKXEXXDXDXC     | 34 |
|    |    | :   :   :   :   :   :   :       |    |
| Dd | 63 | CDICKTVVTEAGNLLKDNATEEILHYLEKTC | 94 |

RESULT 5  
JH0604  
saposin precursor - mouse  
N;Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; component (SAP); sphingolipid activator protein A2; sulfated glycoprotein 1; sulfatide sulfon  
N;Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JH0604  
R;Tsuda, M.; Sakiyama, T.; Endo, H.; Kitagawa, T.  
Biochem. Biophys. Res. Commun. 184, 1266-1272, 1992  
A;Title: The primary structure of mouse saposin.  
A;Reference number: JH0604; MUID:92272718; PMID:1590788  
A;Accession: JH0604  
A;Molecule type: mRNA  
A;Residues: 1-557 <TSU>  
A;Cross-references: GB:S36200; NID:g249386; PIDN:AB22175.1; PID:g249387  
A;Experimental source: liver  
C;Function:  
A;Description: saposins bind sphingolipids, form hydrophilic complexes and make them  
A;Pathway: sphingolipid catabolism  
A;Note: saposins A and C (SAP-2) activate hydrolysis of glucocerebroside by beta-gluc  
A;Note: saposin B (SAP-1) activates hydrolysis of galactocerebroside sulfate by aryls  
A;Note: saposin D activates hydrolysis of sphingomyelin by sphingomyelin phosphodiester  
C;Superfamily: saposin; saposin repeat homology  
C;Keywords: alternative splicing; glycoprotein; lysosomal storage disease; lysosome;  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-557/Product: prosaposin #status predicted <PRO>  
F;55-148/Domain: saposin repeat homology <SAP1>  
F;60-143/Product: saposin A #status predicted <SAPA>  
F;189-283/Domain: saposin repeat homology <SAP2>

[illegible]

F:194-276/Product: saposin B #status predicted <SAP1>  
F:309-400/Domain: saposin repeat homology <SAP3>  
F:313-392/Product: saposin C #status predicted <SAPC>  
F:434-525/Domain: saposin repeat homology <SAP4>  
F:440-517/Product: saposin D #status predicted <SAPD>  
F:63-138,66-132,94-106,197-273,200-267,229-240,317-39  
F:80-1214,334,379,459/Binding site: carbohydrate (Asn)

Query Match 32.8%; Score 43; DB 1; Length 557;  
Best Local Similarity 21.9%; Pred. No. 12;  
Matches 7; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

**QY**      3 CEXCEXXXKEXXXXXNNKKEXXXDXDXC 34  
          | : | : | : | : | : | : | : | : |  
**Dd**      63 CDICKTVVTEAGNLLKDNATOEILHYLEKTC 94

RESULT 6  
T46339  
hypothetical protein DKFZp34A0814.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text  
C:Accession: T46339  
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.;  
submitted to the Protein Sequence Database, January 2000

Query Match 32.8%; Score 43; DB 2; Length 913;  
Best Local Similarity 42.9%; Pred. No. 19;  
Matches 9; Conservative 1; Mismatches 11; Indels

QY 4 EXCEXXXKEXXKXXDNKXK 24  
pB 799 EICEKEKKELKKMKKROEK 819

RESULT 7  
A28822  
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - bovine  
N;Alternate names: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta; phosph  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 22-Jun-1999  
C;Accession: A28822; A39236  
R;Katan, M.; Kriz, R.W.; Totty, N.; Philp, R.; Meldrum, E.; Aldape, R.A.; Knopf, J.L.; H  
Cell 54, 171-177, 1988  
A;Title: Determination of the primary structure of PLC-154 demonstrates diversity of pho  
A;Reference number: A28822; MUID:88270496; PMID:2455601

```

F:539-659/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y
F:887/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experime

Query Match 32.8%; Score 43; DB 2; Length 1216;
Best Local Similarity 42.9%; Pred. NO. 23;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXXKXXDNNKXEK 24
 | | | | | | | | | |
Db 1059 EICEKERKELKKRMDKKRQEK 1079

RESULT 8
A28821
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) I - rat
N;Alternate names: triphosphoinositide phosphodiesterase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: A28821
R;Suh, P.G.; Ryu, S.H.; Moon, K.H.; Suh, H.W.; Rhee, S.G.
Cell 54, 161-169, 1988
A;Title: Cloning and sequence of multiple forms of phospholipase C.
A;Reference number: A90899; MUID:88270495; PMID:3390863

```

Query Match 32.8%; Score 43; DB 2; Length 1216;  
Best Local Similarity 42.9%; Pred. No. 23;  
Matches 9; Conservative 1; Mismatches 11; Indels

|    |      |            |              |      |
|----|------|------------|--------------|------|
| QY | 4    | EXCEXXXXXX | DDNNKXK      | 24   |
|    |      |            |              | :    |
| Dd | 1059 | EICEKEKKEL | KKKKMDKKRQEK | 1079 |

```

RESULT 9
T15674
hypothetical protein C28C12.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: T15674

```

A; map position: 4  
A; Introns: 76/2; 172/3; 210/3; 256/3; 281/3

Query Match 32.1%; Score 42; DB 2; Length 314;  
Best Local Similarity 26.9%; Pred. NO. 11;  
Matches 7; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

**QY** 3 CEXCEXXXXXXNDNNKXEXXD 28  
| : | : || :: | : | -  
**Dp** 215 CDECFWVKELTVVEKKSOAEARD 240





A:Experimental source: strain 168  
C:Genetics:  
A:Gene: yvce

Query Match 31.7%; Score 41.5; DB 2; Length 473;  
Best Local Similarity 40.7%; Pred. No. 19;  
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY 7 EXXXKEXKXXDN-NKXKEXKXXDK 32  
| | : : | : | | | | | |  
DB 52 EAKERTELQENQSKIEKELKDINDK 78

RESULT 14

Tl8450  
hypothetical protein C0570c - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2002  
C:Accession: Tl8450  
R:Lawson, D.; Bowman, S.; Barrell, B.  
submitted to the EMBL Data Library, November 1998  
A:Reference number: Z18937  
A:Accession: Tl8450  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-419 <LAW>  
A:Cross-references: EMBL:AL008970; NID:e1407852; PIDN:CAA15592.1  
C:Genetics:  
A:Map position: 3  
A:Introns: 15/3; 169/1  
A:Note: C0570c

Query Match 31.3%; Score 41; DB 2; Length 419;  
Best Local Similarity 29.0%; Pred. No. 21;  
Matches 9; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXXDNKXKEXKXXDKXC 34  
| | : | | : : | | : : | |  
DB 291 EECKEYKEDCKDECKEEDKCKEKGKKEC 321

RESULT 15

H69472  
iron-dependent repressor homolog - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: H69472  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: H69472  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-191 <KLE>  
A:Cross-references: GB:AE000979; GB:AE000782; NID:g2689302; PIDN:AAB89462.1; PID:g264876  
C:Superfamily: conserved hypothetical protein MJ0568

Query Match 30.5%; Score 40; DB 1; Length 191;  
Best Local Similarity 34.8%; Pred. No. 16;  
Matches 8; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXXDNKXKEXKE 25  
| | | | : | : | | |  
DB 121 CEVCESCTQEYLSLSDATEGEYE 143

Search completed: June 2, 2003, 14:16:20  
Job time : 14.641 secs



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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:13 ; Search time 6.82051 Seconds  
(without alignments)  
231.082 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXCEXXXKEXKXXDNKXKEXKXXDXDXKXCKKXX 38

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 101   | 77.1        | 524    | 1 SAP_HUMAN  | P07602 h proactiva |
| 2          | 87    | 66.4        | 525    | 1 SAP_BOVIN  | P26779 b proactiva |
| 3          | 61    | 46.6        | 81     | 1 SAP_CAVPO  | P20097 cavia porce |
| 4          | 58    | 44.3        | 518    | 1 SAP_CHICK  | O13035 gallus gall |
| 5          | 46    | 35.1        | 554    | 1 SAP_RAT    | P10960 rattus norv |
| 6          | 43    | 32.8        | 557    | 1 SAP_MOUSE  | Q61207 mus musculu |
| 7          | 43    | 32.8        | 1216   | 1 PIB1_BOVIN | P10894 bos taurus  |
| 8          | 43    | 32.8        | 1216   | 1 PIB1_HUMAN | Q9nq66 homo sapien |
| 9          | 43    | 32.8        | 1216   | 1 PIB1_RAT   | P10687 rattus norv |
| 10         | 42    | 32.1        | 483    | 1 CBF5_YEAST | P33322 saccharomyc |
| 11         | 42    | 32.1        | 574    | 1 TACY_STRCB | Q53957 streptococc |
| 12         | 42    | 32.1        | 574    | 1 TACY_STRSQ | Q54114 streptococc |
| 13         | 41.5  | 31.7        | 473    | 1 YVCE_BACSU | P40767 bacillus su |
| 14         | 40    | 30.5        | 519    | 1 YMP4_YEAST | Q04347 saccharomyc |
| 15         | 39    | 29.8        | 189    | 1 YPT2_CAEEL | P41880 caenorhabdi |
| 16         | 39    | 29.8        | 572    | 1 NH25_CAEEL | Q19345 caenorhabdi |
| 17         | 38    | 29.0        | 474    | 1 CBF5_KLULA | O13473 kluyveromyc |
| 18         | 38    | 29.0        | 1048   | 1 Z217_HUMAN | O75362 homo sapien |
| 19         | 38    | 29.0        | 1451   | 1 SPT6_YEAST | P23615 saccharomyc |
| 20         | 37.5  | 28.6        | 489    | 1 Y092_METJA | Q57557 methanococc |
| 21         | 37.5  | 28.6        | 666    | 1 BIP_LYCES  | P49118 lycopersico |
| 22         | 37.5  | 28.6        | 668    | 1 BIP5_TOBAC | Q03685 nicotiana t |
| 23         | 37.5  | 28.6        | 1391   | 1 MST2_DROHY | Q08696 drosophila  |
| 24         | 37    | 28.2        | 238    | 1 NEUM_HUMAN | P17677 homo sapien |
| 25         | 37    | 28.2        | 373    | 1 ACT_CHOCR  | P53499 chondrus cr |
| 26         | 37    | 28.2        | 375    | 1 DEK_HUMAN  | P35659 homo sapien |
| 27         | 37    | 28.2        | 472    | 1 ZIM3_HUMAN | Q96pe6 homo sapien |
| 28         | 37    | 28.2        | 524    | 1 YBY8_YEAST | P38277 saccharomyc |
| 29         | 37    | 28.2        | 846    | 1 CLOC_HUMAN | O15516 homo sapien |
| 30         | 37    | 28.2        | 855    | 1 CLOC_MOUSE | O08785 mus musculu |
| 31         | 37    | 28.2        | 886    | 1 HS97_STRFN | Q94738 strongyloce |
| 32         | 36.5  | 27.9        | 668    | 1 BIP2_ARATH | Q39043 arabidopsis |
| 33         | 36.5  | 27.9        | 669    | 1 BIP1_ARATH | Q91kr3 arabidopsis |

RESULT 1

SAP\_HUMAN

| ID | SAP_HUMAN                                                             | STANDARD;                                               | PRT; | 524 AA |
|----|-----------------------------------------------------------------------|---------------------------------------------------------|------|--------|
| AC | P07602;                                                               | P07292; P15793; P78538; P78546; P78547; Q92741; Q92742; |      |        |
| AC | Q92740;                                                               | Q92739; P78541; P78558;                                 |      |        |
| DT | 01-APR-1988                                                           | (Rel. 07, Created)                                      |      |        |
| DT | 01-APR-1990                                                           | (Rel. 14, Last sequence update)                         |      |        |
| DT | 15-JUN-2002                                                           | (Rel. 41, Last annotation update)                       |      |        |
| DE | Proactivator polypeptide precursor                                    | [Contains: Saposin A (Protein A);                       |      |        |
| DE | Saposin B (Sphingolipid activator protein 1)                          | (SAP-1) (Cerebroside                                    |      |        |
| DE | sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);     |                                                         |      |        |
| DE | Saposin C (Co-beta-glucosidase) (A1 activator) (Glucosylceramidase    |                                                         |      |        |
| DE | activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D      |                                                         |      |        |
| DE | (Protein C) (Component C)].                                           |                                                         |      |        |
| GN | PSAP.                                                                 |                                                         |      |        |
| OS | Homo sapiens (Human).                                                 |                                                         |      |        |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                                                         |      |        |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.           |                                                         |      |        |
| OX | NCBI_TaxID=9606;                                                      |                                                         |      |        |
| RN | [1]                                                                   |                                                         |      |        |
| RP | SEQUENCE FROM N.A.                                                    |                                                         |      |        |
| RC | TISSUE=Liver;                                                         |                                                         |      |        |
| RX | MEDLINE=90129043; PubMed=2515150;                                     |                                                         |      |        |
| RA | Rorman E.G., Grabowski G.A.;                                          |                                                         |      |        |
| RT | "Molecular cloning of a human co-beta-glucosidase cDNA: evidence that |                                                         |      |        |
| RT | four sphingolipid hydrolase activator proteins are encoded by single  |                                                         |      |        |
| RT | genes in humans and rats.";                                           |                                                         |      |        |
| RL | Genomics 5:486-492(1989).                                             |                                                         |      |        |
| RN | [2]                                                                   |                                                         |      |        |
| RP | SEQUENCE FROM N.A.                                                    |                                                         |      |        |
| RX | MEDLINE=89255151; PubMed=2498298;                                     |                                                         |      |        |
| RA | Nakano T., Sandhoff K., Stuenkel J., Christomanou H., Suzuki K.;      |                                                         |      |        |
| RT | "Structure of full-length cDNA coding for sulfatide activator, a      |                                                         |      |        |
| RT | Co-beta-glucosidase and two other homologous proteins: two alternate  |                                                         |      |        |
| RT | forms of the sulfatide activator.";                                   |                                                         |      |        |
| RL | J. Biochem. 105:152-154(1989).                                        |                                                         |      |        |
| RN | [3]                                                                   |                                                         |      |        |
| RP | SEQUENCE FROM N.A.                                                    |                                                         |      |        |
| RC | TISSUE=Eye, and Skin;                                                 |                                                         |      |        |
| RA | Strausberg R.;                                                        |                                                         |      |        |
| RL | Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.               |                                                         |      |        |
| RN | [4]                                                                   |                                                         |      |        |
| RP | SEQUENCE OF 59-125 AND 304-513 FROM N.A.                              |                                                         |      |        |
| RC | TISSUE=Brain;                                                         |                                                         |      |        |
| RX | MEDLINE=91192146; PubMed=2013321;                                     |                                                         |      |        |
| RA | Holtschmidt H., Sandhoff K., Fuerst W., Kwon H.Y., Schnabel D.,       |                                                         |      |        |
| RA | Suzuki K.;                                                            |                                                         |      |        |
| RT | "The organization of the gene for the human cerebroside sulfate       |                                                         |      |        |
| RT | activator protein.";                                                  |                                                         |      |        |
| RL | FEBS Lett. 280:267-270(1991).                                         |                                                         |      |        |
| RN | [5]                                                                   |                                                         |      |        |
| RP | SEQUENCE OF 164-524 FROM N.A.                                         |                                                         |      |        |
| RX | MEDLINE=88068647; PubMed=2825202;                                     |                                                         |      |        |
| RA | Dewji N.N., Wenger D.A., O'Brien J.S.;                                |                                                         |      |        |
| RT | "Nucleotide sequence of cloned cDNA for human sphingolipid activator  |                                                         |      |        |
| RT | protein 1 precursor.";                                                |                                                         |      |        |

ALIGNMENTS

RL Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).  
RN [6]  
RP PARTIAL SEQUENCE OF 60-142.  
RX MEDLINE=89240739; PubMed=2717620;  
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,  
RA Kishimoto Y.;  
RT "Saposin A: second cerebroside activator protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).  
RN [7]  
RP SEQUENCE OF 195-263 FROM N.A.  
RX MEDLINE=86130593; PubMed=2868718;  
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,  
RA Hill F., O'Brien J.S.;  
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),  
RT the sulfatide sulfatase activator.";  
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).  
RN [8]  
RP SEQUENCE OF 195-274.  
RX TISSUE=Kidney;  
RA MEDLINE=9106165; PubMed=2209618;  
RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;  
RT "The complete amino-acid sequences of human ganglioside GM2 activator  
RT protein and cerebroside sulfate activator protein.";  
RL Eur. J. Biochem. 192:709-714(1990).  
RN [9]  
RP SEQUENCE OF 195-274.  
RX MEDLINE=89207118; PubMed=3242555;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence of the naturally occurring A2 activator  
RT protein for enzymic sphingomyelin degradation: identity to the  
RT sulfatide activator protein (SAP-1).";  
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).  
RN [10]  
RP SEQUENCE OF 311-390.  
RX MEDLINE=88163077; PubMed=3442600;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence and carbohydrate content of the  
RT naturally occurring glucosylceramide activator protein (A1 activator)  
RT absent from a new human Gaucher disease variant.";  
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).  
RN [11]  
RP SEQUENCE OF 407-484.  
RX MEDLINE=89000190; PubMed=3048308;  
RA Furst W., Machleidt W., Sandhoff K.;  
RT "The precursor of sulfatide activator protein is processed to three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).  
RN [12]  
RP PARTIAL SEQUENCE OF 405-484.  
RX MEDLINE=89025876; PubMed=2845979;  
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;  
RT "Saposin D: a sphingomyelinase activator.";  
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).  
RN [13]  
RP SEQUENCE OF 17-26.  
RC TISSUE=Milk;  
RX MEDLINE=92068206; PubMed=1958198;  
RA Kondoh K., Hinenio T., Sano A., Kakimoto Y.;  
RT "Isolation and characterization of prosaposin from human milk.";  
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).  
RN [14]  
RP PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.  
RC TISSUE=Urine;  
RX MEDLINE=20032116; PubMed=10562467;  
RA Fluaharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,  
RA Waring A.J., To T., Fluaharty C.B., Faull K.F.;  
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)  
RT from human urine.";  
RL Mol. Genet. Metab. 68:391-403(1999).  
RN [15]  
RP STRUCTURE OF CARBOHYDRATE ON ASN-215.  
RX MEDLINE=2110404; PubMed=11180632;  
RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,

RA Stevens R.L., Fluaharty C.B., Fluaharty A.L.;  
RT "Structure of the asparagine-linked sugar chains of porcine kidney and  
RT human urine cerebroside sulfate activator protein.";  
RL J. Mass Spectrom. 35:1416-1424(2000).  
RN [16]  
RP MASS SPECTROMETRY.  
RC TISSUE=Urine;  
RX MEDLINE=99441404; PubMed=10510427;  
RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,  
RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,  
RA Fluaharty C.B., Fluaharty A.L.;  
RT "Cerebroside sulfate activator protein (Saposin B): chromatographic  
RT and electrospray mass spectrometric properties.";  
RL J. Mass Spectrom. 34:1040-1054(1999).  
RN [17]  
RP VARIANT MLD ILE-217.  
RX MEDLINE=90147748; PubMed=2302219;  
RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
RT mRNA in patients with a variant form of metachromatic  
RT leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
RN [18]  
RP SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.  
RX MEDLINE=90207231; PubMed=2320574;  
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluaharty A.L.,  
RA O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
RT deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
RN [19]  
RP VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=91210267; PubMed=2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
RA Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
RT three mRNAs and a newly found mutation responsible for a clinical  
RT disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
RN [20]  
RP VARIANT GAUCHER PHE-388.  
RX MEDLINE=91285107; PubMed=2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
RT variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
RN [21]  
RP REVIEW ON MLD VARIANTS.  
RX MEDLINE=95170731; PubMed=7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place  
CC by the sequential action of specific hydrolases. Some of these  
CC enzymes require specific low-molecular mass, non-enzymic proteins:  
CC the sphingolipids activator proteins (coproteins).  
CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
CC Saposin C apparently acts by combining with the enzyme and acidic  
CC lipid to form an activated complex, rather than by solubilizing  
CC the substrate.  
CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and  
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
CC Saposin B forms a solubilizing complex with the substrates of the  
CC sphingolipid hydrolases.  
CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
CC activator (EC 3.1.4.12).  
CC -!- SUBUNIT: Saposin B is a homodimer.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),

Query Match 77.1%; Score 101; DB 1; Length 524;  
Best Local Similarity 55.9%; Pred. No. 1.le-09;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXDNNKXKEXXDXDXKXCK 36  
II II II I IIII III I III I  
Db 315 CEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCK 348

RESULT 2  
SAP\_BOVIN  
ID SAP\_BOVIN STANDARD; PRT; 525 AA.  
AC P26779; Q9N2G4;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Proactivator polypeptide precursor [Contains: Saposin A (Protein A);  
Saposin B (Sphingolipid activator protein 1) (SAP-1) (Cerebroside  
sulfate activator) (CSAct) (Dispersin) (Sulfatide/GM1 activator);  
Saposin C (Co-beta-glucosidase) (Al activator) (Glucosylceramidase  
activator) (Sphingolipid activator protein 2) (SAP-2); Saposin D  
(Protein C) (Component C)].  
GN PSAP.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A., AND VARIANTS.  
RC TISSUE=Mammary gland;  
RA Azuma N., Yoshida K.;  
RT "RT-PCR cloning of bovine prosaposin.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 312-391.  
RC TISSUE=Spleen;  
RX MEDLINE=92207994; PubMed=1554743;  
RA Sano A., Mizuno T., Kondoh K., Hineno T., Ueno S.-I., Kakimoto Y.,  
Morita N.;  
RT "Saposin-C from bovine spleen; complete amino acid sequence and  
relation between the structure and its biological activity.";  
RL Biochim. Biophys. Acta 1120:75-80(1992).  
CC -|- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE  
BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE  
ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:  
THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).  
-|- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF  
GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND  
GLACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).  
SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC  
LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING  
THE SUBSTRATE.  
-|- FUNCTION: SAPOSIN B STIMULATES THE HYDROLYSIS OF GALACTO-  
CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1  
GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND  
GLOBOTRIAOSYLCERAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).  
SAPOSIN B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE  
SPHINGOLIPID HYDROLASES (BY SIMILARITY).  
-|- FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE  
ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).  
-|- SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).  
-|- SUBCELLULAR LOCATION: Lysosomal.  
-|- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL  
PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID  
HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).  
-|- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.  
-|- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.  
-----  
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-----  
DR EMBL; AB036791; BAA95677.1; -  
DR PIR; S21770; S21770.  
DR InterPro; IPR003119; Sapa.  
DR InterPro; IPR000004; SapaB.  
DR Pfam; PF02199; Sapa; 2.  
DR ProDom; PD001732; SapaB; 4.  
DR SMART; SM00162; Sapa; 2.  
DR SMART; SM00118; SapaB; 4.  
KW Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 60 142 SAPOSIN A.  
FT CHAIN 196 275 SAPOSIN B.  
FT CHAIN 312 392 SAPOSIN C.  
FT CHAIN 406 487 SAPOSIN D.  
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.  
FT DOMAIN 59 142 SAPOSIN-LIKE TYPE B 1.  
FT DOMAIN 194 276 SAPOSIN-LIKE TYPE B 2.  
FT DOMAIN 312 393 SAPOSIN-LIKE TYPE B 3.  
FT DOMAIN 406 487 SAPOSIN-LIKE TYPE B 4.  
FT DOMAIN 492 525 SAPOSIN-LIKE TYPE A 2.  
FT DISULFID 63 138 BY SIMILARITY.  
FT DISULFID 66 132 BY SIMILARITY.  
FT DISULFID 94 106 BY SIMILARITY.  
FT DISULFID 199 272 BY SIMILARITY.  
FT DISULFID 202 266 BY SIMILARITY.  
FT DISULFID 231 242 BY SIMILARITY.  
FT DISULFID 316 389 BY SIMILARITY.  
FT DISULFID 319 383 BY SIMILARITY.  
FT DISULFID 347 358 BY SIMILARITY.  
FT DISULFID 410 483 BY SIMILARITY.  
FT DISULFID 413 477 BY SIMILARITY.  
FT DISULFID 441 452 BY SIMILARITY.  
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 216 216 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 427 427 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARIANT 127 127 H -> R.  
FT VARIANT 260 263 MQPK -> IRIR.  
FT CONFLICT 317 317 E -> Q (IN REF. 2).  
FT CONFLICT 367 367 R -> S (IN REF. 1).  
SQ SEQUENCE 525 AA; 58120 MW; 293AFC0FB9C4FA99 CRC64;  
Query Match 66.4%; Score 87; DB 1; Length 525;  
Best Local Similarity 47.1%; Pred. No. 2.3e-07;  
Matches 16; Conservative 2; Mismatches 16; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXDNNKXKEXXDXDXKXCK 36  
II II II I IIII III I III I  
Db 316 CEVCEFLVKEVAKLIDNNRTEELHALDKVCSK 349

RESULT 3  
SAP\_CAVPO  
ID SAP\_CAVPO STANDARD; PRT; 81 AA.  
AC P20097;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Saposin C (CO-beta-glucosidase) (Glucosylceramidase activator)  
DE (Sphingolipid activator protein 2) (SAP-2).  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Hystriognathia; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;

```
RX MEDLINE-89066787; PubMed-3198642;
RA Sano A., Radin N.S., Johnson L.L., Tarr G.E.;
RT "The activator protein for glucosylceramide beta-glucosidase from
RT guinea pig liver. Improved isolation method and complete amino acid
RT sequence."
RL J. Biol. Chem. 263:19597-19601(1988).
CC -1- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCERAMIDE BY BETA-GALACTOSYLCERAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE.
CC -1- SIMILARITY: CONTAINS 1 SAPOSIN B-TYPE DOMAIN.
CC PIR; A32026; A32026.
DR HSSP; P42210; IQDM.
DR InterPro; IPR000004; SapB.
DR ProDom; PD001732; SapB; 1.
DR SMART; SM00118; SAPB; 1.
KW Glycoprotein; Sphingolipid metabolism.
FT DOMAIN 1 81 SAPOSIN-LIKE TYPE B.
FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .).
FT DISULFID 5 78 BY SIMILARITY.
FT DISULFID 8 72 BY SIMILARITY.
FT DISULFID 36 47 BY SIMILARITY.
SQ SEQUENCE 81 AA; 8852 MW; E564CE1F0A292596 CRC64;

Query Match 46.6%; Score 61; DB 1; Length 81;
Best Local Similarity 31.2%; Pred. No. 0.00084;
Matches 10; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXXDNNKXKEXXDXDXKXC 34
Db 5 CKACEYVVKVMELIDNRRTEKIIHALDSVC 36

RESULT 4
SAP_CHICK STANDARD; PRT; 518 AA.
AC O13035;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Proactivator polypeptide precursor [Contains: Saposin A; Saposin B;
DE Saposin C; Saposin D].
GN PSAP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 194-203.
RC TISSUE=Brain, and Liver;
RX MEDLINE-98129745; PubMed-9461526;
RA Azuma N., Seo H.-C., Lie O., Fu Q., Gould R.M., Hiraiwa M., Burt D.W.,
RA Paton I.R., Morrice D.R., O'Brien J.S., Kishimoto Y.;
RL "Cloning, expression and map assignment of chicken prosaposin.";
RN Blochem. J. 330:321-327(1998).
RP [2]
RA SEQUENCE FROM N.A.
RA Altman N., Horowitz M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE LYSOSOMAL DEGRADATION OF SPHINGOLIPIDS TAKES PLACE
CC BY THE SEQUENTIAL ACTION OF SPECIFIC HYDROLASES. SOME OF THESE
CC ENZYMES REQUIRE SPECIFIC LOW-MOLECULAR MASS, NON-ENZYMIC PROTEINS:
CC THE SPHINGOLIPIDS ACTIVATOR PROTEINS (COPROTEINS) (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN A AND SAPOSIN C STIMULATE THE HYDROLYSIS OF
CC GLUCOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.45) AND
CC GALACTOSYLCERAMIDE BY BETA-GLUCOSYLCERAMIDASE (EC 3.2.1.46).
CC SAPOSIN-C APPARENTLY ACTS BY COMBINING WITH THE ENZYME AND ACIDIC
CC LIPID TO FORM AN ACTIVATED COMPLEX, RATHER THAN BY SOLUBILIZING
CC THE SUBSTRATE (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN B STIMULATES THE HYDROLYSIS OF GALACTO-
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CC CEREBROSIDE SULFATE BY ARYLSULFATASE A (EC 3.1.6.8), GM1
CC GANGLIOSIDES BY BETA-GALACTOSIDASE (EC 3.2.1.23) AND
CC GLOBOTRIAOSYLCERAMIDE BY ALPHA-GALACTOSIDASE A (EC 3.2.1.22).
CC SAPOSIN-B FORMS A SOLUBILIZING COMPLEX WITH THE SUBSTRATES OF THE
CC SPHINGOLIPID HYDROLASES (BY SIMILARITY).
CC -1- FUNCTION: SAPOSIN D IS A SPECIFIC SPHINGOMYELIN PHOSPHODIESTERASE
CC ACTIVATOR (EC 3.1.4.12) (BY SIMILARITY).
CC -1- SUBUNIT: SAPOSIN B IS A HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -1- PTM: THIS PRECURSOR IS PROTEOLYTICALLY PROCESSED TO 4 SMALL
CC PEPTIDES, WHICH ARE SIMILAR TO EACH OTHER AND ARE SPHINGOLIPID
CC HYDROLASE ACTIVATOR PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB003471; BAA19914.1; -
DR EMBL; AF108656; AAF05899.1; -
DR InterPro; IPR003119; SapA.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 4.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
KW Signal; Glycoprotein; Lysosome; Sphingolipid metabolism; Repeat;
KW GM2-gangliosidosis.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 61 143 SAPOSIN A.
FT CHAIN 194 276 SAPOSIN B.
FT CHAIN 307 387 SAPOSIN C.
FT CHAIN 399 480 SAPOSIN D.
FT DOMAIN 22 55 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 60 143 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 193 277 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 307 388 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 399 480 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 485 518 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 64 139 BY SIMILARITY.
FT DISULFID 67 133 BY SIMILARITY.
FT DISULFID 95 107 BY SIMILARITY.
FT DISULFID 197 273 BY SIMILARITY.
FT DISULFID 200 267 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 311 384 BY SIMILARITY.
FT DISULFID 314 378 BY SIMILARITY.
FT DISULFID 342 353 BY SIMILARITY.
FT DISULFID 403 476 BY SIMILARITY.
FT DISULFID 406 470 BY SIMILARITY.
FT DISULFID 434 445 BY SIMILARITY.
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 420 420 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 94 94 R -> T (IN REF. 2).
FT CONFLICT 486 486 E -> D (IN REF. 2).
SQ SEQUENCE 518 AA; 57601 MW; B803000E891C3963 CRC64;

Query Match 44.3%; Score 58; DB 1; Length 518;
Best Local Similarity 34.4%; Pred. No. 0.015;
Matches 11; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXXDNNKXKEXXDXDXKXC 34
Db 311 CEICETMVKEVTGLLESNKTEEEIVHEMEVVC 342
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Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXXDNKKXK 24  
 ||| ||| | : |||  
 Db 1059 EICEKEKKELKKMKKKRQEK 1079

RESULT 8  
 PIB1\_HUMAN  
 ID PIB1\_HUMAN STANDARD; PRT; 1216 AA.  
 AC Q9NQ66; Q9NQ65; Q9NQH9; Q9NTH4; Q60325; Q9H4H2; Q9BQW2; Q9UJJP6;  
 AC Q9UM26;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1  
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC-154).  
 GN PLCB1 OR KIAA0581.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).  
 RC TISSUE=Brain;  
 RX PubMed=11118617;  
 RA Caricasole A., Sala C., Roncarati R., Formenti E., Terstappen G.C.;  
 RT "Cloning and characterization of the human phosphoinositide-specific  
 RT phospholipase C-beta 1 (PLCbeta1).";  
 RL Biochim. Biophys. Acta 1517:63-72(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=Brain;  
 RX MEDLINE=20225428; PubMed=10760467;  
 RA Peruzzi D., Calabrese G., Faenza I., Manzoli L., Matteucci A.;  
 RA Gianfrancesco F., Billi A.M., Stuppia L., Palka G., Cocco L.;  
 RT "Identification and chromosomal localisation by fluorescence in situ  
 RT hybridisation of human gene of phosphoinositide-specific phospholipase  
 RT C beta 1.";  
 RL Biochim. Biophys. Acta 1484:175-182(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharaslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [4]  
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).  
 RC TISSUE=Testis;

RA Koehler K., Beyer A., Mewes H.-W., Gassenhuber J., Wiemann S.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).  
 RC TISSUE=Brain;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES  
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS  
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE  
 CC C ENZYMES.  
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-  
 CC bisphosphate + H(2)O = D-myo-inositol 1,4,5-trisphosphate +  
 CC diacylglycerol.  
 CC -1- COFACTOR: Calcium.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS  
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.  
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS  
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; AJ278313; CAB98142.1; -;  
 DR EMBL; AJ278314; CAB98143.1; -;  
 DR EMBL; AY004175; AAF86613.1; -;  
 DR EMBL; AL031683; CAC16181.1; -;  
 DR EMBL; AL031683; CAC34366.1; -;  
 DR EMBL; AL050315; CAB56498.1; -;  
 DR EMBL; AL049632; CAB46663.1; -;  
 DR EMBL; AL137267; CAB70666.1; -;  
 DR EMBL; AB011153; BAA25507.1; -;  
 DR HSSP; P10688; 1DJX.  
 DR Genew; HGNC:15917; PLCB1.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR001192; PI\_PLC.  
 DR InterPro; IPR000909; PI\_PLC\_xdom.  
 DR InterPro; IPR001711; PI\_PLC\_Y.  
 DR Pfam; PF00168; C2; 2.  
 DR Pfam; PF00387; PI-PLC-Y; 3.  
 DR Pfam; PF00388; PI-PLC-X; 2.  
 DR PRINTS; PR00390; PHPLIPASEC.  
 DR ProDom; PD001202; PI\_PLC\_Y; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00148; PLCXC; 1.  
 DR SMART; SM00149; PLCYC; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 1.  
 DR PROSITE; PS50007; PIPLC\_X\_DOMAIN; 1.  
 DR PROSITE; PS50008; PIPLC\_Y\_DOMAIN; 1.  
 KW Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium;  
 KW Alternative splicing.  
 FT DOMAIN 316 467 DOMAIN X.  
 FT DOMAIN 540 656 DOMAIN Y.  
 FT DOMAIN 663 761 C2 DOMAIN.  
 FT ACT\_SITE 331 331 BY SIMILARITY.  
 FT ACT\_SITE 378 378 BY SIMILARITY.  
 FT MOD\_RES 887 887 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 FT VARSPPLIC 1142 1216 LOVELEYQDKFKRLPLEILEFFQKAMKISDSNHGSA  
 FT PLSSSDPGKVNHRKTPSSEELGGDIPGKFDTP -> GEG  
 FT SSSFLSECHEDPSVSPNFTPPNPQALKW (IN ISOFORM

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FT CONFLICT 1 34 MAGAOPGVHALQKPCVSDSLKKGTFKVKWDD -> MGS
FT CONFLICT 189 189 L -> M (IN REF. 2).
FT CONFLICT 203 203 P -> L (IN REF. 2).
FT CONFLICT 216 216 L -> F (IN REF. 2).
FT CONFLICT 221 221 P -> L (IN REF. 2).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT CONFLICT 309 309 P -> T (IN REF. 2).
FT CONFLICT 320 320 Q -> R (IN REF. 2).
FT CONFLICT 352 352 V -> A (IN REF. 2).
FT CONFLICT 366 366 K -> R (IN REF. 2).
FT CONFLICT 393 393 E -> K (IN REF. 2).
FT CONFLICT 983 983 P -> S (IN REF. 1; CAB98143).
SQ SEQUENCE 1216 AA; 138566 MW; 6F4263DIA50C6FD1 CRC64;

Query Match 32.8%; Score 43; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXXXDNNKXK 24
| | | | | | | | | |
Db 1059 EICEKELKKKKMDKKRQEK 1079

RESULT 9
PIBL_RAT
ID PIBL_RAT STANDARD; PRT; 1216 AA.
AC P10687;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-1) (PLC-154).
GN PLCB1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88270495; PubMed=3390863;
RA Suh P.-G., Ryu S.H., Moon K.H., Suh H.W., Rhee S.G.;
RT "Cloning and sequence of multiple forms of phospholipase C.";
RL Cell 54:161-169(1988).
RN [2]
RP ACTIVITY, TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RX MEDLINE=93203266; PubMed=8454637;
RA Jhon D.-Y., Lee H.-H., Park D., Lee C.-W., Lee K.-H., Yoo O.J.,
RA Rhee S.G.;
RT "Cloning, sequencing, purification, and Gq-dependent activation of
RT phospholipase C-beta 3.";
RL J. Biol. Chem. 268:6654-6661(1993).
CC -|- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -|- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -|- COFACTOR: Calcium.
CC -|- SUBCELLULAR LOCATION: Cytosolic and particulate fractions.
CC -|- TISSUE SPECIFICITY: Highest expression in brain. Also expressed in
CC parotid gland, liver, uterus, lung, heart, adrenal gland and
CC ovary. Not detected in spleen, pancreas, intestine, thymus or
CC kidney.
CC -|- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
CC -|- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -|- SIMILARITY: CONTAINS 1 C2 DOMAIN.

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DR EMBL; M20636; AJA41885.1; -.
DR PIR; A28821; A28821.
DR HSP; P10688; IDJX.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_xdom.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
KW Hydrolase; Lipid degradation; Transducer; Phosphorylation; Calcium.
FT DOMAIN 316 467 DOMAIN X.
FT DOMAIN 540 656 DOMAIN Y.
FT DOMAIN 663 761 C2 DOMAIN.
FT ACT_SITE 331 331 BY SIMILARITY.
FT ACT_SITE 378 378 BY SIMILARITY.
FT MOD_RES 887 887 PHOSPHORYLATION (BY PKC).
SQ SEQUENCE 1216 AA; 138344 MW; 92F23691781F788E CRC64;

Query Match 32.8%; Score 43; DB 1; Length 1216;
Best Local Similarity 42.9%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXXXDNNKXK 24
| | | | | | | | | |
Db 1059 EICEKELKKKKMDKKRQEK 1079

RESULT 10
CBF5_YEAST
ID CBF5_YEAST STANDARD; PRT; 483 AA.
AC P33322;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Centromere/microtubule binding protein CBF5 (Centromere-binding factor
DE 5) (Nucleolar protein CBF5) (P64').
GN CBF5 OR YLR175W OR L9470.11.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=93330283; PubMed=8336724;
RA Jiang W., Middleton K., Yoon H.-J., Fouquet C., Carbon J.;
RT "An essential yeast protein, CBF5p, binds in vitro to centromeres and
RT microtubules.";
RL Mol. Cell. Biol. 13:4884-4893(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D.,
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CC -----

DR EMBL; D16824; BAA04104.1; -.  
DR HSSP; P19995; 1PFO.  
DR InterPro; IPR001869; Thiol\_cytolysin.  
DR Pfam; PF01289; Thiol\_cytolysin; 1.  
DR PRINTS; PR01400; TACYTOLYSIN.  
DR PRODOM; PD007062; Thiol\_cytolysin; 1.  
DR PROSITE; PS00481; THIOI\_CYTOLYSINS; 1.  
KW Toxin; Hemolysis; Cytolysis; Signal.  
FT SIGNAL 1 36 BY SIMILARITY.  
FT CHAIN 37 574 STREPTOLYSIN O.  
FT ACT\_SITE 533 533 BINDING TO CHOLESTEROL (BY SIMILARITY).  
SQ SEQUENCE 574 AA; 63992 MW; 83345CEBDELEBCFC CRC64;

Query Match 32.1%; Score 42; DB 1; Length 574;  
Best Local Similarity 36.4%; Pred. No. 7.4;  
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 EXXXKEXKXXDNKXKEXXD 28  
| | | | | | | | | | :  
DB 89 ESAEKEKKSEDNKKSEEDHTE 110

RESULT 13  
YVCE\_BACSU STANDARD; PRT; 473 AA.  
AC P40767; O06969;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein yvce (PSPA2).  
GN YVCE.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RA Denizot F.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 1-71 FROM N.A.  
RX MEDLINE=89108019; Pubmed=3145906;  
RA Smith H., de Jong A., Bron S., Venema G.;  
RT "Characterization of signal-sequence-coding regions selected from the  
RT Bacillus subtilis chromosome.";  
RL Gene 70:351-361(1988).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C40.  
CC -----

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DR EMBL; Z94043; CAB08053.1; -.  
DR EMBL; Z99121; CAB15485.1; -.  
DR EMBL; M22901; AAA22817.1; ALT\_FRAME.  
DR Subtilist; BG11023; yvce.  
DR InterPro; IPR000064; NLPC\_P60.  
DR Pfam; PF00877; NLPC\_P60; 1.  
KW Hypothetical protein; Complete proteome.  
FT ACT\_SITE 377 377 POTENTIAL.  
SQ SEQUENCE 473 AA; 51033 MW; AF544B030E683038 CRC64;

Query Match 31.7%; Score 41.5; DB 1; Length 473;

Best Local Similarity 40.7%; Pred. No. 7.5;  
Matches 11; Conservative 3; Mismatches 12; Indels 1; Gaps 1;  
QY 7 EXXXKEXKXXDN-NKXKEXKXXDK 32  
| | | | | | | | | | :  
DB 52 EAKEKEITELQENQSKIEKELKDINDK 78

RESULT 14  
YMP4\_YEAST STANDARD; PRT; 519 AA.  
AC Q04347;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Hypothetical 60.1 kDa protein in SEC59-ERG5 intergenic region.  
GN YMR014W OR YN9711.01.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / AB972;  
RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
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DR EMBL; Z49211; CAA89115.1; -.  
DR SGD; S0004616; YMR014W.  
KW Hypothetical protein; Coiled coil.  
FT DOMAIN 426 486 COILED COIL (POTENTIAL).  
SQ SEQUENCE 519 AA; 60054 MW; 8142768058BFA264 CRC64;

Query Match 30.5%; Score 40; DB 1; Length 519;  
Best Local Similarity 27.6%; Pred. No. 14;  
Matches 8; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXKXXDNKXKEXKXXDK 32  
| | | | | | | | | | :  
DB 464 EASRSRERDRRTETNNKKEESASTGEE 492

RESULT 15  
YPT2\_CAEEL STANDARD; PRT; 189 AA.  
AC P41880;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Hypothetical 21.6 kDa protein F37A4.2 in chromosome III.  
GN F37A4.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Fulton L., Waterston R.;  
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.  
CC -----

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DR EMBL; U00032; AAA50630.1; -.  
DR WormPep; F37A4.2; CE00710.  
KW Hypothetical protein.  
SQ SEQUENCE 189 AA; 21602 MW; 8827BCC630A015D4 CRC64;

Query Match 29.8%; Score 39; DB 1; Length 189;  
Best Local Similarity 36.4%; Pred. No. 8.3;  
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 EXXXXKXXXXDNNKXEXXD 28  
I I: : I: I I I I  
Db 160 ESEGKQNTVEEDKDKVEKETD 181

Search completed: June 2, 2003, 14:14:39  
Job time : 9.32051 secs







```
AC Q9DGH7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Prosaposin.
GN PSAP.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Altman N., Horowitz M.;
RT *The zebrafish prosaposin cDNA.*;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108655; AAG32919.1; -.
DR ZFIN; ZDB-GENE-020108-1; psap.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 3.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
SQ SEQUENCE 522 AA; 57671 MW; D3C15A305725C1CD CRC64;

Query Match 34.4%; Score 45; DB 13; Length 522;
Best Local Similarity 28.1%; Pred. No. 7.5;
Matches 9; Conservative 2; Mismatches 21; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXXDNNKXEXXDXDXKXC 34
Db 314 CAICEYVMKEIENMIQDTSEAEIQAQVKVC 345

RESULT 3
Q97322 PRELIMINARY; PRT; 1334 AA.
AC Q97322;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 160.8 kDa protein.
GN PFC1010W, MAL3P7.32.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT *The complete nucleotide sequence of chromosome 3 of Plasmodium
RT falciparum.*;
RL Nature 400:532-538(1999).
DR EMBL; AL034559; CAB39073.2; -.
KW Hypothetical protein.
SQ SEQUENCE 1334 AA; 160847 MW; E3577E84C7E0C8E5 CRC64;

Query Match 33.6%; Score 44; DB 5; Length 1334;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 10; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 7 EXXXKEXXXDNNKXEXXDXDXKXCXK 36
Db 887 EDMKKEKWKYENNNNNKDKNKNCCLK 916
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RESULT 4
Q9DGH7 PRELIMINARY; PRT; 285 AA.
AC Q9DGH7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Fas ligand receptor soluble form (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT *Fas Expression and Regulation in Hen Granulosa Cells.*;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF296875; AAG02243.1; -.
DR HSSP; O14763; 1D4V.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 285 AA; 32431 MW; A9761960CCD79E6D CRC64;

Query Match 33.2%; Score 43.5; DB 13; Length 285;
Best Local Similarity 31.2%; Pred. No. 8.1;
Matches 10; Conservative 2; Mismatches 15; Indels 5; Gaps 1;

QY 3 CEXCEXXXKEXXXDNNKXEXXDXDXKXC 34
Db 85 CEHCESCT-----VCENGQIEKECTSTSDTVC 111

RESULT 5
Q9DGH8 PRELIMINARY; PRT; 312 AA.
AC Q9DGH8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fas antigen (Fragment).
GN FAS.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgman J.T., Johnson A.L.;
RT *Fas Expression and Regulation in Hen Granulosa Cells.*;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF296874; AAG02242.1; -.
DR HSSP; O14763; 1D4V.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
```

```
FT NON_TER 1 1
SQ SEQUENCE 312 AA; 35275 MW; 5496BCF1E4CE676C CRC64;

Query Match
Best Local Similarity 33.2%; Score 43.5; DB 13; Length 312;
Matches 10; Conservative 2; Mismatches 15; Indels 5; Gaps 1;

QY 3 CEXCEXXXKEXXXDNNKXEXXDXDXKXC 34
 ||||| :||| |
Db 85 CEHCESCT-----VCENGQIEKECTSTSDTVC 111

RESULT 6
Q9Z0E5 PRELIMINARY; PRT; 1173 AA.
AC Q9Z0E5;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Phospholipase C-beta-1B'.
GN PLCB1 OR PLCB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SWISS 3T3;
RA Wu K., Bai J., Marks D.L., Pagano R.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SWISS 3T3;
RA Wu K., Bai J., Marks D.L., Pagano R.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SWISS 3T3;
RA Wu K., Bai J., Marks D.L., Machamer C., Pagano R.E.;
RT "Cloning of PI-Specific Phospholipase C's from 3T3 Cells.##I.
RT Expression and Membrane Targeting of a Novel Phospholipase C-beta-1
RT isoform.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U85714; AAD00573.1; -.
DR EMBL; U85713; AAD00572.1; -.
DR HSSP; P10688; 1DJX.
DR MGD; MGI:97613; Plcbl.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI-PLC.
DR InterPro; IPR000909; PI-PLC_xdom.
DR InterPro; IPR001711; PI-PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI-PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1173 AA; 133255 MW; D2F5F00BE9785FFC CRC64;

Query Match
Best Local Similarity 32.8%; Score 43; DB 11; Length 1173;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXXXDNNKXEXK 24
 ||||| :||| |
Db 1059 EICEKEKKELKKMDKKRQEK 1079

RESULT 7
Q9Z1B3 PRELIMINARY; PRT; 1216 AA.
AC Q9Z1B3;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
```

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DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Phospholipase C-beta-1a.
GN PLCB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SWISS 3T3;
RA Wu K., Bai J., Marks D.L., Pagano R.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U85712; AAD00571.1; -.
DR HSSP; P10688; 1DJX.
DR MGD; MGI:97613; Plcbl.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001192; PI-PLC.
DR InterPro; IPR000909; PI-PLC_xdom.
DR InterPro; IPR001711; PI-PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI-PLC-X; 1.
DR Pfam; PF00387; PI-PLC-Y; 1.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI-PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1216 AA; 138324 MW; D873078A58CE824D CRC64;

Query Match
Best Local Similarity 32.8%; Score 43; DB 11; Length 1216;
Matches 9; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 4 EXCEXXXKEXXXDNNKXEXK 24
 ||||| :||| |
Db 1059 EICEKEKKELKKMDKKRQEK 1079

RESULT 8
Q9YLS1 PRELIMINARY; PRT; 52 AA.
AC Q9YLS1;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hexon protein (Fragment).
GN HEXON.
OS Human adenovirus type 5.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95355;
RX MEDLINE=99143271; PubMed=9986873;
RA Li Q.G., Henningsson A., Juto P., Elgh F., Wadell G.;
RT "Use of restriction fragment analysis and sequencing of a serotype-
RT specific region to type adenovirus isolates.";
RL J. Clin. Microbiol. 37:844-847(1999).
DR EMBL; AF051949; AAD18129.1; -.
DR HSSP; P03277; 1DHX.
DR InterPro; IPR000736; Adeno_hexon.
DR Pfam; PF01065; Adeno_hexon; 1.
DR ProDom; PD002815; Adeno_hexon; 1.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5776 MW; CA787840339C61DC CRC64;

Query Match
Best Local Similarity 32.1%; Score 42; DB 12; Length 52;
Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 4;
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DR HSSP; P19995; 1PFO.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACTOLYSIN.
DR ProDom; PD007062; Thiol_cytolysin; 1.
DR PROSITE; PS00481; THIOI_CYTOLYSINS; 1.
SQ SEQUENCE 574 AA; 64026 MW; 8336FEEBDE1A5CFC CRC64;

Query Match 32.1%; Score 42; DB 2; Length 574;
Best Local Similarity 36.4%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 EXXXKEXKXXDNNKXKEXXD 28
Db 89 ESAEKEKKSEDNKKSEEDHTE 110

RESULT 12
Q9QUG2 PRELIMINARY; PRT; 852 AA.
AC Q9QUG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE DINB1 (DNA polymerase kappa).
GN POLK OR DINB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=TESTIS;
RA Ogi T., Kato T., Jr., Kato T., Ohmori H.;
RT "Mutation enhancement by DINB1, a mammalian homologue of the
RT Escherichia coli mutagenesis protein DinB.";
RL Genes Cells 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99449784; PubMed=10518552;
RA Gerlach V.L., Aravind L., Gotway G., Schultz R.A., Koonin E.V.,
RA Friedberg E.C.;
RT "Human and mouse homologs of Escherichia coli DinB (DNA polymerase
RT IV), members of the UmuC/DinB superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:11922-11927(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Ogi T., Ohmori H.;
RT "Mouse DNA polymerase kappa gene, exon14-15.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB027563; BAA86942.1; -
DR EMBL; AF163571; AAF02541.1; -
DR EMBL; AB040765; BAB59059.1; -
DR EMBL; AB040753; BAB59059.1; JOINED.
DR EMBL; AB040754; BAB59059.1; JOINED.
DR EMBL; AB040755; BAB59059.1; JOINED.
DR EMBL; AB040756; BAB59059.1; JOINED.
DR EMBL; AB040757; BAB59059.1; JOINED.
DR EMBL; AB040758; BAB59059.1; JOINED.
DR EMBL; AB040759; BAB59059.1; JOINED.
DR EMBL; AB040760; BAB59059.1; JOINED.
DR EMBL; AB040761; BAB59059.1; JOINED.
DR EMBL; AB040762; BAB59059.1; JOINED.
DR EMBL; AB040763; BAB59059.1; JOINED.
DR EMBL; AB040764; BAB59059.1; JOINED.
DR MGD; MGI:1349767; Polk.
DR InterPro; IPR001126; UMUC_like.
DR Pfam; PF00817; INS; 1.
SQ SEQUENCE 852 AA; 96002 MW; FDBF33A6E78992F4 CRC64;

Query Match 32.1%; Score 42; DB 11; Length 852;
Best Local Similarity 41.2%; Pred. No. 37;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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QY 18 DNNKXEXKXXDXDKXC 34
Db 715 ENNRSEKCPDIPDKSC 731

RESULT 13
O15997 PRELIMINARY; PRT; 965 AA.
AC O15997;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Bmp109.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278844; PubMed=9611271;
RA Tambunan J., Chang P.-K., Li H., Natori M.;
RT "Molecular cloning of a cDNA encoding a silkworm protein which
RT contains the conserved BH regions of Bcl-2 family proteins.";
RL Gene 212:287-293(1998).
DR EMBL; AB008449; BAA23126.1; -
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR000004; SapaB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapaB; 6.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SapaB; 7.
SQ SEQUENCE 965 AA; 108825 MW; F41A7BEE7F626078 CRC64;

Query Match 32.1%; Score 42; DB 5; Length 965;
Best Local Similarity 25.0%; Pred. No. 41;
Matches 8; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXKXXDNNKXKEXKXXDXDKXC 34
Db 877 CAVCETVVMVAVKKVLEKLDNRNIVHIIKSC 908

RESULT 14
O64046 PRELIMINARY; PRT; 2285 AA.
AC O64046;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transglycosylase.
GN YOMI.
OS Bacteriophage SPBC2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=66797;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Maue C.,
RA Karamata D.;
RT "The complete nucleotide sequence of the Bacillus subtilis SPbetac2
RT prophage.";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020713; AAC13005.1; -
DR HSSP; P00718; 153L.
DR InterPro; IPR002886; Peptidase_M37.
DR InterPro; IPR000189; SLT_domain.
DR Pfam; PF01551; Peptidase_M37; 1.
DR Pfam; PF01464; SLT; 1.
DR PROSITE; PS00922; TRANSGLYCOSYLASE; 1.
SQ SEQUENCE 2285 AA; 252310 MW; FF602C227754B357 CRC64;

Query Match 32.1%; Score 42; DB 9; Length 2285;
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Best Local Similarity 38.5%; Pred. No. 87;  
Matches 10; Conservative 1; Mismatches 15; Indels 0; Gaps 0;  
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Db 881 EDASKEIKSKDELKQYKQIADYNDK 906

RESULT 15  
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ID O31976 PRELIMINARY; PRT; 2285 AA.  
AC O31976;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE YOMI protein.  
GN YOMI.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
OC Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,  
RA Borriess R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillette S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the gram-positive bacterium Bacillus  
RT subtilis.";  
RL Nature 390:249-256(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=168;  
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;  
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; 299115; CAB14053.1; -.  
DR HSSP; P00718; 153L.  
DR InterPro; IPR002886; Peptidase\_M37.  
DR InterPro; IPR000189; SLT\_domain.  
DR Pfam; PF01551; Peptidase\_M37; 1.  
DR Pfam; PF01464; SLT; 1.  
DR PROSITE; PS00922; TRANSGLYCOSYLASE; 1.  
KW Complete proteome.  
SQ SEQUENCE 2285 AA; 252310 MW; FF602C227754B357 CRC64;

Query Match 32.1%; Score 42; DB 16; Length 2285;  
Best Local Similarity 38.5%; Pred. No. 87;

Matches 10; Conservative 1; Mismatches 15; Indels 0; Gaps 0;  
QY 7 EXXXKEXKXXDNNKXKEXKEXDXXDK 32  
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Db 881 EDASKEIKSKDELKQYKQIADYNDK 906  
Search completed: June 2, 2003, 14:17:19  
Job time : 27.3462 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:14:43 ; Search time 11.6923 Seconds  
(without alignments)  
95.624 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XCCEXCEXXXKEXXKXNDNKKXEXXDXDXKXCKXKX 38

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID               | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 101   | 77.1        | 80     | 1 US-08-100-247-3   | Sequence 3, Appli  |
| 2          | 101   | 77.1        | 80     | 1 US-08-483-146A-3  | Sequence 3, Appli  |
| 3          | 101   | 77.1        | 80     | 1 US-08-232-513A-4  | Sequence 4, Appli  |
| 4          | 101   | 77.1        | 80     | 1 US-08-484-594A-3  | Sequence 3, Appli  |
| 5          | 101   | 77.1        | 523    | 1 US-08-100-247-2   | Sequence 2, Appli  |
| 6          | 101   | 77.1        | 523    | 1 US-08-483-146A-2  | Sequence 2, Appli  |
| 7          | 101   | 77.1        | 523    | 1 US-08-232-513A-3  | Sequence 3, Appli  |
| 8          | 101   | 77.1        | 523    | 1 US-08-484-594A-2  | Sequence 2, Appli  |
| 9          | 61    | 46.6        | 22     | 1 US-08-100-247-1   | Sequence 1, Appli  |
| 10         | 61    | 46.6        | 22     | 1 US-08-483-146A-1  | Sequence 1, Appli  |
| 11         | 61    | 46.6        | 22     | 1 US-08-232-513A-1  | Sequence 1, Appli  |
| 12         | 61    | 46.6        | 22     | 1 US-08-484-594A-1  | Sequence 1, Appli  |
| 13         | 61    | 46.6        | 22     | 4 US-09-231-159-1   | Sequence 1, Appli  |
| 14         | 61    | 46.6        | 22     | 4 US-08-611-307-1   | Sequence 1, Appli  |
| 15         | 61    | 46.6        | 22     | 4 US-09-148-030-1   | Sequence 1, Appli  |
| 16         | 56    | 42.7        | 22     | 4 US-09-231-159-8   | Sequence 8, Appli  |
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| 19         | 54    | 41.2        | 22     | 1 US-08-232-513A-18 | Sequence 18, Appli |
| 20         | 54    | 41.2        | 22     | 1 US-08-484-594A-9  | Sequence 9, Appli  |
| 21         | 54    | 41.2        | 22     | 4 US-09-231-159-7   | Sequence 7, Appli  |
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| 23         | 50    | 38.2        | 18     | 1 US-08-100-247-5   | Sequence 5, Appli  |
| 24         | 50    | 38.2        | 18     | 1 US-08-483-146A-5  | Sequence 5, Appli  |
| 25         | 50    | 38.2        | 18     | 1 US-08-232-513A-6  | Sequence 6, Appli  |
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| 28 | 50 | 38.2 | 18   | 4 US-08-611-307-20  | Sequence 20, Appli |
| 29 | 50 | 38.2 | 18   | 4 US-09-148-030-2   | Sequence 2, Appli  |
| 30 | 45 | 34.4 | 15   | 4 US-09-148-030-10  | Sequence 10, Appli |
| 31 | 42 | 32.1 | 14   | 4 US-09-231-159-10  | Sequence 10, Appli |
| 32 | 42 | 32.1 | 14   | 4 US-08-611-307-10  | Sequence 10, Appli |
| 33 | 42 | 32.1 | 2285 | 4 US-09-308-375-2   | Sequence 2, Appli  |
| 34 | 38 | 29.0 | 12   | 4 US-09-231-159-3   | Sequence 3, Appli  |
| 35 | 38 | 29.0 | 12   | 4 US-08-611-307-3   | Sequence 3, Appli  |
| 36 | 38 | 29.0 | 12   | 4 US-09-148-030-3   | Sequence 3, Appli  |
| 37 | 38 | 29.0 | 15   | 4 US-09-148-030-9   | Sequence 9, Appli  |
| 38 | 38 | 29.0 | 22   | 1 US-08-483-146A-8  | Sequence 8, Appli  |
| 39 | 38 | 29.0 | 22   | 1 US-08-232-513A-17 | Sequence 17, Appli |
| 40 | 38 | 29.0 | 22   | 1 US-08-484-594A-8  | Sequence 8, Appli  |
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| 43 | 37 | 28.2 | 662  | 4 US-09-405-728-3   | Sequence 3, Appli  |
| 44 | 37 | 28.2 | 846  | 3 US-08-885-291-55  | Sequence 55, Appli |
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ALIGNMENTS

RESULT 1  
US-08-100-247-3  
; Sequence 3, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: O'BRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; CLONE: SAPOSIN C  
US-08-100-247-3

Query Match 77.1%; Score 101; DB 1; Length 80;  
Best Local Similarity 55.9%; Pred. No. 2.2e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;









ANTI-SENSE: NO  
FRAGMENT TYPE: Internal  
IMMEDIATE SOURCE:  
CLONE: 22-MER FRAGMENT  
US-08-100-247-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXKE 25  
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Db 1 CEFLVKEVTKLIDNNKTE 20

## RESULT 10

US-08-483-146A-1  
; Sequence 1, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Blvd. 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,146A  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned A  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: MYELOS.002DV1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal

## US-08-483-146A-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXKE 25  
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Db 1 CEFLVKEVTKLIDNNKTE 20

## RESULT 11

US-08-483-146A-1  
; Sequence 1, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Blvd. 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,146A  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelson, Ned A  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: MYELOS.002DV1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-235-8550  
TELEFAX: 619-235-0176  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal

## US-08-483-146A-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

US-08-232-513A-1  
; Sequence 1, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.

; TITLE OF INVENTION: ProsaPOSIN and Cytokine-Derived Peptides  
; TITLE OF INVENTION: as Therapeutic Agents  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,513A  
FILING DATE: 21-APR-1994

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/100,247  
FILING DATE: 30-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1643  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY: Peptide  
LOCATION: 1..22  
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Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXKE 25  
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Db 1 CEFLVKEVTKLIDNNKTE 20

RESULT 12  
US-08-484-594A-1  
; Sequence 1, Application US/08484594A  
; Patent No. 5714459  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES  
; TITLE OF INVENTION: DERIVED THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Drive, Sixteenth Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,513A  
FILING DATE: 21-APR-1994

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/100,247  
FILING DATE: 30-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 1643  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY: Peptide  
LOCATION: 1..22  
OTHER INFORMATION: /label= SapC

## US-08-232-513A-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXKXXDNNKXKE 25  
|| || | |||| ||||  
Db 1 CEFLVKEVTKLIDNNKTE 20

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,594A  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/100,247  
;; FILING DATE: 30-JUL-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Israelsen, Ned A  
;; REGISTRATION NUMBER: 29,655  
;; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-235-8550  
;; TELEFAX: 619-235-0176  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-484-594A-1

Query Match 46.6%; Score 61; DB 1; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20

## RESULT 13

US-09-231-159-1  
; Sequence 1, Application US/09231159  
; Patent No. 6268347  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; CLASSIFICATION:  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE: 05-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949

;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 22 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-09-231-159-1

Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20

## RESULT 14

US-08-611-307-1  
; Sequence 1, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611;307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-611-307-1

Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXE 25  
|| || | |||| |||  
Db 1 CEFLVKEVTKLIDNNKTE 20

## RESULT 15

US-09-148-030-1  
; Sequence 1, Application US/09148030C  
; Patent No. 6458357  
; GENERAL INFORMATION:  
; APPLICANT: White, Michael T.  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Wright, David E.  
; TITLE OF INVENTION: RETRO-INVERSO NEUROTROPHIC AND ANALGESIC

; TITLE OF INVENTION: PEPTIDES  
; FILE REFERENCE: MYELOS.004CPI  
; CURRENT APPLICATION NUMBER: US/09/148,030C  
; CURRENT FILING DATE: 1998-09-03  
; PRIOR APPLICATION NUMBER: 08/926,015  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-148-030-1

Query Match 46.6%; Score 61; DB 4; Length 22;  
Best Local Similarity 60.0%; Pred. No. 0.00032;  
Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXKE 25  
  ||  ||  |  ||||  |||  
Db 1 CEFVKEVTKLIDNNKTEKE 20

Search completed: June 2, 2003, 14:18:24  
Job time : 13.1923 secs







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; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-780-438A-1

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Query Match 77.1%; Score 101; DB 9; Length 40;  
Best Local Similarity 55.9%; Pred. No. 2.9e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels

|    |   |                                    |    |
|----|---|------------------------------------|----|
| Qy | 3 | CEXCEXXXKEEXXXXXNNNKEKEEXDXXDKXCK  | 36 |
|    |   |                                    |    |
| Db | 5 | CEVCEFLVKEVTKLLIDNNKTEKEILLDAFDKMC | 38 |

### RESULT 3

US-09-767-007A-3  
; Sequence 3, Application US/09767007A  
; Patent No. US20020077275A1

```

; GENERIC INFORMATION.
; APPLICANT: John S. O'Brien
; APPLICANT: yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
; US-09-767-007A-3

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|                          |        |                    |        |            |
|--------------------------|--------|--------------------|--------|------------|
| Query Match              | 77.1%; | Score 101;         | DB 10; | Length 80; |
| Best Local Similarity    | 55.9%; | Pred. No. 5.7e-10; |        |            |
| Matches 19; Conservative | 0;     | Mismatches 15;     | Indels |            |

[illegible]

## RESULT 4

US-09-753-126-3  
; Sequence 3, Application US/09753126  
; Patent No. US20020127219A1

; GENERAL INFORMATION.  
 ; APPLICANT: OKKELS, JENS SIGURD  
 ; APPLICANT: JENSEN, ANNE DAM  
 ; APPLICANT: HALKIER, TORBEN  
 ; APPLICANT: JENSEN, RIKKE BOLDING  
 ; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME  
 ; TITLE OF INVENTION: ACTIVATORS  
 ; FILE REFERENCE: 31-0006000S  
 ; CURRENT APPLICATION NUMBER: US/09/753,126  
 ; CURRENT FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: PA 1999 01891  
 ; PRIOR FILING DATE: 1999-12-30  
 ; PRIOR APPLICATION NUMBER: 60/174,652  
 ; PRIOR FILING DATE: 2000-01-06  
 ; PRIOR APPLICATION NUMBER: PA 200 00865  
 ; PRIOR FILING DATE: 2000-06-02  
 ; PRIOR APPLICATION NUMBER: 60/210,984  
 ; PRIOR FILING DATE: 2000-06-12

```

; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn ver. 2.1

```

Query Match 77.1%; Score 101; DB 10; Length 80;  
Best Local Similarity 55.9%; Pred. No. 5.7e-10;  
Matches 19; Conservative 0; Mismatches 15; Indels

|           |          |                                                                   |           |
|-----------|----------|-------------------------------------------------------------------|-----------|
| <b>QY</b> | <b>3</b> | C E X E X X K E X X X X D N N K X E K E X X D X D K X C X K       | <b>36</b> |
|           |          |                                                                   |           |
| <b>Dd</b> | <b>5</b> | C E V C F L V K E V T K L I D N N K T E K E I L D A F D K M C S K | <b>38</b> |

## RESULTS

US-10-043-487-340  
; Sequence 340, Application US/10043487  
; Publication No. US20030055220A1

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/ CARRIER INFORMATION:
/ APPLICANT: HYBRIGENICS
/ APPLICANT: Pierre, LEGRAIN
/ TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep
/ TITLE OF INVENTION: mammalian polypeptides
/ FILE REFERENCE: B4778A
/ CURRENT APPLICATION NUMBER: US/10/043,487
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/261,130
/ PRIOR FILING DATE: 2001-01-12
/ NUMBER OF SEQ ID NOS: 561
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 340
/ LENGTH: 209

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Query Match 77.1%; Score 101; DB 9; Length 209;  
Best Local Similarity 55.9%; Pred. No. 1.5e-09;  
Matches 19: Conservative 0; Mismatches 15; Indels

QY 3 CEXCEXXXKEXXXDNNKXEXEXDXDXKXCK 36  
 165 CEVCEFLVKEVTKLIDNNKTEKEILDAFDCMSK 198

## RESULT 6

US-09-767-007A-2  
; Sequence 2, Application US/09767007A  
; Patent No. US20020077275A1

```

/ APPLICANT: John S. O'Brien
/ APPLICANT: Yasuo Kishimoto
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
/ TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
/ FILE REFERENCE: MYELOS.2DC1C1
/ CURRENT APPLICATION NUMBER: US/09/767,007A
/ CURRENT FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: 08/958,970
/ PRIOR FILING DATE: 1997-10-28
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 523
/ TYPE: PRT

```

```

; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-73

Query Match 77.1%; Score 101; DB 9; Length 527;
Best Local Similarity 55.9%; Pred. No. 3.6e-09;
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 3 CEXCEXXXKEXXKXXDNKNXKEKEXDXDXDKXCXK 36
 ||||| || | |||| |||| | |||||
DB 318 CEVCFELVKETKLIDNNKTEKEILDADFDMCSK 351

RESULT 10
US-09-753-126-4
; Sequence 4, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSSOMAL ENZYMES AND LYSSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: SapC-linker-GCB polypeptide
US-09-753-126-4

Query Match 77.1%; Score 101; DB 10; Length 592;
Best Local Similarity 55.9%; Pred. No. 4.1e-09;
Matches 19; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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| Qy | 3 | C E X C E X X K E X X X D N N K X E K E X X D X Y D K X C X K       | 36 |
|    |   |                                                                     |    |
| Db | 5 | C E V C E F L V K E V T K L I D N N K T E K E I L D A F D K M C S K | 38 |

RESULT 11  
US-09-767-007A-1  
; Sequence 1, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-1

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RESULT 12
US-09-957-143-1
; Sequence 1, Application US/09957143
; Patent No. US20020128193A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: David E. Wright
; TITLE OF INVENTION: RETRO-INVERSO PROSAPOSIN-DERIVED
; TITLE OF INVENTION: PEPTIDES AND USE THEREOF
; FILE REFERENCE: MYELOS.018C1
; CURRENT APPLICATION NUMBER: US/09/957,143
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: PCT/US00/08550
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/126,991
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-957-143-1

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RESULT 13  
US-09-767-007A-9  
; Sequence 9, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: Yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-9

RESULT 14  
US-09-767-007A-5  
; Sequence 5, Application US/09767007A  
; Patent No. US20020077275A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: yasuo Kishimoto  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPIC PEPTIDES DERIVED THEREFROM  
; FILE REFERENCE: MYELOS.2DC1C1  
; CURRENT APPLICATION NUMBER: US/09/767,007A  
; CURRENT FILING DATE: 2001-01-22  
; PRIOR APPLICATION NUMBER: 08/958,970  
; PRIOR FILING DATE: 1997-10-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial peptide  
US-09-767-007A-5

RESULT 15  
US-09-957-143-2  
; Sequence 2, Application US/09957143  
; Patent No. US20020128193A1  
; GENERAL INFORMATION:  
; APPLICANT: John S. O'Brien  
; APPLICANT: David E. Wright

;; TITLE OF INVENTION: RETRO-INVERSO PROSAPO SIN- DERIVED  
;; TITLE OF INVENTION: PEPTIDES AND USE THEREOF  
;; FILE REFERENCE: MYELOS.018C1  
;; CURRENT APPLICATION NUMBER: US/09/957,143  
;; CURRENT FILING DATE: 2001-09-19  
;; PRIOR APPLICATION NUMBER: PCT/US00/08550  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: 60/126,991  
;; PRIOR FILING DATE: 1999-03-30  
;; NUMBER OF SEQ ID NOS: 10  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 2  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide  
US-09-957-143-2

Query Match 38.2%; Score 50; DB 10; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.039;  
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 11 KEXXXDNNKXKE 25  
||| |  
Db 2 KEVTKLIDNNKTEKE 16

Search completed: June 2, 2003, 14:17:53  
Job time : 15.1026 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2003, 14:15:48 ; Search time 35 Seconds.  
(without alignments)  
144.672 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXCEXXXKEXXXDNNKXKEXXXDXXKXXKXX 38

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 131   | 100.0       | 80     | AA70784  | Saposin-C. Homo s  |
| 2          | 131   | 100.0       | 80     | AAW85653 | Human saposin C.   |
| 3          | 131   | 100.0       | 80     | AAU05697 | Human Saponin C, S |
| 4          | 131   | 100.0       | 523    | AAU05697 | Amino acid sequenc |
| 5          | 131   | 100.0       | 524    | AA70783  | Prosaposin. Homo   |
| 6          | 131   | 100.0       | 524    | AAW85652 | Human prosaposin N |
| 7          | 131   | 100.0       | 524    | AAU58716 | Human prosaposin.  |
| 8          | 131   | 100.0       | 527    | AAU58716 | Amino acid sequenc |
| 9          | 131   | 100.0       | 592    | AAU05698 | Human glucocerebro |
| 10         | 85    | 64.9        | 25     | AAU67289 | Human saposin C.   |

|    |      |      |      |    |          |                     |
|----|------|------|------|----|----------|---------------------|
| 11 | 77   | 58.8 | 22   | 16 | AA70773  | Saposin-C neurotro  |
| 12 | 77   | 58.8 | 22   | 18 | AAW30013 | Prosaposin-derived  |
| 13 | 77   | 58.8 | 22   | 19 | AAW66127 | Prosaposin recepto  |
| 14 | 77   | 58.8 | 22   | 20 | AAW85656 | Prosaposin recepto  |
| 15 | 77   | 58.8 | 22   | 22 | AAW67305 | Peptide #5. Homo    |
| 16 | 76   | 58.0 | 21   | 21 | AAW82281 | Human saposin C 22  |
| 17 | 74   | 56.5 | 340  | 22 | ABG22055 | Novel human diagno  |
| 18 | 72   | 55.0 | 22   | 18 | AAW30028 | Mutant human prosa  |
| 19 | 72   | 55.0 | 22   | 19 | AAW66134 | Prosaposin derivat  |
| 20 | 71   | 54.2 | 25   | 22 | AAW67293 | Bovine saposin C.   |
| 21 | 71   | 54.2 | 744  | 22 | ABW62930 | Drosophila melanog  |
| 22 | 70   | 53.4 | 22   | 18 | AAW30018 | Bovine prosaposin-  |
| 23 | 70   | 53.4 | 22   | 19 | AAW66133 | Prosaposin recepto  |
| 24 | 70   | 53.4 | 22   | 20 | AAW85661 | Prosaposin recepto  |
| 25 | 70   | 53.4 | 554  | 23 | ABB57102 | Mouse ischaemic co  |
| 26 | 70   | 53.4 | 953  | 22 | ABB58389 | Drosophila melanog  |
| 27 | 69   | 52.7 | 567  | 22 | AAW39351 | Human polypeptide   |
| 28 | 69   | 52.7 | 571  | 22 | AAW41137 | Human polypeptide   |
| 29 | 68   | 51.9 | 2285 | 20 | AAW98149 | Bacillus subtilis   |
| 30 | 67   | 51.1 | 324  | 22 | ABG05001 | Novel human diagno  |
| 31 | 66.5 | 50.8 | 540  | 22 | ABB59403 | Drosophila melanog  |
| 32 | 66   | 50.4 | 459  | 22 | ABG21310 | Novel human diagno  |
| 33 | 66   | 50.4 | 1036 | 23 | ABB93295 | Herbicideally activ |
| 34 | 65.5 | 50.0 | 666  | 22 | ABG12052 | Novel human diagno  |
| 35 | 65.5 | 50.0 | 1058 | 22 | AAW80177 | Human protein SEQ   |
| 36 | 65.5 | 50.0 | 1216 | 22 | AAW79193 | Human lipid metabo  |
| 37 | 65.5 | 50.0 | 1216 | 23 | ABB08204 | Drosophila melanog  |
| 38 | 65   | 49.6 | 578  | 22 | ABB71910 | Novel human diagno  |
| 39 | 65   | 49.6 | 851  | 22 | ABG07753 | Human lipoprotein   |
| 40 | 65   | 49.6 | 951  | 22 | AAW97182 | Human phospholipas  |
| 41 | 64.5 | 49.2 | 134  | 22 | ABB11113 | Arabidopsis thalia  |
| 42 | 64.5 | 49.2 | 144  | 21 | AAG09966 | Arabidopsis thalia  |
| 43 | 64.5 | 49.2 | 144  | 21 | AAG50454 | Human Fas antigen   |
| 44 | 64.5 | 49.2 | 159  | 18 | AAW50288 | Arabidopsis thalia  |
| 45 | 64.5 | 49.2 | 165  | 21 | AAG09965 | Arabidopsis thalia  |

ALIGNMENTS

RESULT 1

AA70784

ID AA70784 standard; Protein; 80 AA.

XX

AC AA70784;

XX

DT 30-AUG-1995 (first entry)

XX

DE Saposin-C.

XX

KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;

KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;

KW adrenal leukodystrophy.

XX

OS Homo sapiens.

XX

PN W09503821-A.

XX

PD 09-FEB-1995.

XX

PF 28-JUL-1994; 94WO-US08453.

XX

PR 30-JUL-1993; 93US-0100247.

XX

PR 21-APR-1994; 94US-0232513.

 XX |

PA (OBRI/) OBRIEN J S.

 XX |

PI Kishimoto Y, Obrien JS;

 XX |

DR WPI; 1995-082029/11.

 XX |

PT Stimulating neural cell out-growth and myelination - with

PT pro:saposin, saposin C or new neurotrophic peptide(s) from





Best Local Similarity 50.0%; Pred. No. 0.00059;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCEXXXKEXXXDNNKXEXXDXDXKXXKXX 38  
Db 313 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 6  
AAW85652  
ID AAW85652 standard; Protein; 524 AA.  
XX AAW85652;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE Human prosaposin N-terminal peptide.  
XX  
KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9912559-A1.  
XX  
PD 18-MAR-1999.  
XX  
PF 09-SEP-1998; 98WO-US19216.  
XX  
PR 04-JUN-1998; 98US-0088129.  
PR 09-SEP-1997; 97US-0058352.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI O'brien JS;  
XX  
DR WPI; 1999-229139/19.  
DR N-PSDB; AAX08488.  
XX  
PT Use of prosaposin receptor agonist  
XX  
PS Claim 7; Figure 2; 90pp; English.  
XX

Prosaposin is a 70kDa glycoprotein which is proteolytically processed to generate saposins A, B, C and D, all of which are similar to each other and have a similar placement of six cysteines, a glycosylation site and conserved proline residues. Prosaposin, saposin C and prosaposin derived peptides (prosaptides), have therapeutic applications in promoting recovery after toxic, traumatic, myocardial ischaemic, degenerative and inherited lesions to the peripheral and central nervous system. Prosaposin receptor agonists (PRAs) inhibit proinflammatory cytokine-induced apoptosis by activation of the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2 family members, such as BAD-Bcl-2, releasing Bcl-2 and its family members which inhibit caspases, thereby inhibiting apoptosis. An additional mechanism whereby PRAs inhibit apoptosis is by blocking activation of JNK, a proapoptotic signaling component. Within several minutes after binding to the receptor, PRAs block JNK activation induced by tumor necrosis factor-alpha (TNF alpha). The activation of JNK by TNF alpha is another well known mechanism for TNF alpha-induced, as well as other proinflammatory cytokine-induced apoptosis. The method can be used for inhibiting apoptosis which is

CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Parkinson's disease,  
CC amyotrophic lateral sclerosis, Huntington's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This 524 N-terminal peptide of prosaposin also acts  
CC as a prosaposin receptor agonist.  
XX  
SQ Sequence 524 AA;

Query Match 100.0%; Score 131; DB 20; Length 524;  
Best Local Similarity 50.0%; Pred. No. 0.00059;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCEXXXKEXXXDNNKXEXXDXDXKXXKXX 38  
Db 313 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 7  
AAW58716  
ID AAY58716 standard; Protein; 524 AA.  
XX  
AC AAY58716;  
XX 25-APR-2000 (first entry)  
XX Human prosaposin.  
DE  
XX  
KW Prosaposin; saponin B; antiangiogenic; angiogenesis inhibitor;  
KW antitumour; antiproliferative; antimigratory; Kaposi's sarcoma;  
KW tumour; human; therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Protein 195..275  
FT /note= "mature saposin B"  
FT Peptide 195..205  
FT /note= "specifically claimed antiangiogenic peptide  
FT of Claim 23"  
FT Peptide 196..200  
FT /note= "specifically claimed antiangiogenic peptide  
FT of Claim 4"  
XX  
PN WO200002902-A1.  
XX  
PD 20-JAN-2000.  
XX  
PF 12-JUL-1999; 99WO-US15772.  
XX  
PR 13-JUL-1998; 98US-0092647.  
XX  
PA (GILL/) GILL P S.  
XX  
PI GILL PS;  
XX  
DR WPI; 2000-171128/15.  
XX  
PT Saposin B derived peptides, useful as inhibitors of angiogenesis and  
XX tumor growth -  
PS Disclosure; Page 18; 78pp; English.  
XX  
CC The present sequence is that of human prosaposin, a precursor of  
CC saposin B. The invention is based on the discovery that saposin B,  
CC previously known to be involved in the hydrolysis of sphingolipids,

CC has potent antiangiogenic and antitumour activity, and also has  
CC antiproliferative and antimigratory activity against endothelial  
CC cells. This activity is conserved in cryptic polypeptides as small  
CC as 5 amino acids (see AAY58684-715), which can be synthetically  
CC prepared and used in vitro or in vivo for the treatment of  
CC undesired angiogenesis and tumor growth, especially Kaposi's sarcoma  
CC (claimed). The polypeptides can also be used in conjunction with  
CC cytotoxic moieties to selectively kill certain cell types, e.g. for  
CC treatment of cancer, angiofibroma, neovascular glaucoma,  
CC arteriovenous malformation, nonunion fracture, arthritis and other  
CC connective tissue disorders, Osler-Weber syndrome, atherosclerotic  
CC plaque, psoriasis, corneal graft neovascularization, pyogenic  
CC granuloma, retrolental fibroplasia, diabetic retinopathy,  
CC scleroderma, haemangioma, trachoma, vascular adhesions and  
CC hypertrophic scars.

XX Sequence 524 AA;  
SQ

Query Match 100.0%; Score 131; DB 21; Length 524;  
Best Local Similarity 50.0%; Pred. No. 0.00059;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECEXXXKEXXXDNNKXKEXXXDXXDXKXX 38  
Db 313 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 350

RESULT 8  
AAB31915  
ID AAB31915 standard; Protein; 527 AA.  
XX  
AC AAB31915;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Amino acid sequence of a human protein.  
XX  
KW Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200105422-A2.  
XX  
PD 25-JAN-2001.  
XX  
PF 17-JUL-2000; 2000WO-FR02057.  
XX  
PR 15-JUL-1999; 99FR-0009372.  
XX  
PA (INMR ) BIOMERIEUX STELHYS.  
XX  
PI Roeklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
XX  
DR WPI; 2001-159475/16.  
XX  
PT Detecting, preventing and treating degenerative, neurological and  
PT autoimmune diseases, particularly multiple sclerosis, using specified  
PT polypeptides or related nucleic acid or ligand -  
XX  
PS Claim 1; Page 172-173; 209pp; French.  
XX  
CC The present sequence represents a human protein, which is used in the  
CC method of the invention. The specification describes a method which uses  
CC at least one polypeptide or polynucleotide sequence belonging to the  
CC perlecan, precursor of the retinol-binding plasma protein, precursor of  
CC the ganglioside GM2 activator, calgranulin B or saposin B protein  
CC families. The method is used for detecting, preventing or treating a  
CC degenerative, neurological and/or auto-immune disease. The  
CC polynucleotides and polypeptides are used for diagnosis, prognosis,

CC prevention and treatment of multiple sclerosis (in its various forms  
CC and phases). They may also be useful in cases of e.g. Alzheimer's and  
CC Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid  
CC polyarthritis and lupus erythematosus, including use as vaccines and  
CC in gene therapy (expression of sense or antisense sequences). They can  
CC also be used to assess efficacy of potential therapeutic agents,  
CC particularly compounds that reduce or inhibit toxicity towards glial  
CC cells.

XX  
SQ Sequence 527 AA;  
Query Match 100.0%; Score 131; DB 22; Length 527;  
Best Local Similarity 50.0%; Pred. No. 0.0006;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECEXXXKEXXXDNNKXKEXXXDXXDXKXX 38  
Db 316 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCKSLP 353

RESULT 9  
AAU05698  
ID AAU05698 standard; Protein; 592 AA.  
XX  
AC AAU05698;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human glucocerebrosidase, GCB-Saponin C, SapC, fusion protein.  
XX  
KW Human; glucocerebrosidase; GCB; lysosomal storage disease;  
KW Gaucher's disease; Fabry's disease; Farber's disease;  
KW G\_m\_1 gangliosidosis; Tay-Sach's disease; Niemann-Pick disease;  
KW Shindler disease; Hunter syndrome; Sly syndrome; Huler syndrome;  
KW Scheie syndrome; fusion protein; Saponin C; SapC.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX  
FH Key Location/Qualifiers  
FT Protein 1..80  
FT Peptide /label= SapC  
FT Protein 81..95  
FT Peptide /label= Linker\_peptide  
FT Protein 96..592  
FT Modified-site /label= GCB  
FT Modified-site 114  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 154  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 241  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 365  
FT Modified-site /note= "N-glycosylated"  
XX  
PN WO200149830-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 29-DEC-2000; 2000WO-DK00743.  
XX  
PR 30-DEC-1999; 99DK-0001891.  
PR 02-JUN-2000; 2000DK-0000865.  
PR 02-JUN-2000; 2000DK-0000866.  
PR 30-JUN-2000; 2000DK-0001027.  
XX  
PA (MAXY-) MAXYGEN APS.  
XX  
PI Okkels JS, Jensen AD, Halkier T, Jensen RB, Schambye HT;  
XX WPI; 2001-465259/50.  
XX  
PT Improved lysosomal enzymes and lysosomal enzyme activators useful for

PT treating Gaucher's disease -  
XX Example 5; Page 96-97; 97pp; English.  
PS  
CC The sequence is a fusion protein of human lysosomal enzyme  
CC glucocerebrosidase, GCB and its co-factor, Saponin C, SapC.  
CC GCB is the enzyme involved in Gaucher's disease, a lysosomal  
CC storage disease. The invention relates to introducing new glycosylation  
CC sites into lysosomal enzymes/activators like GCB to improve their  
CC bioactivity. The novel polypeptides are used for the prevention and  
CC treatment of Gaucher's disease, Fabry's disease, Farber's disease,  
CC G<sub>M</sub>1 gangliosidosis, Tay-Sach's disease, Niemann-Pick disease, Shindler  
CC disease, Hunter syndrome, Sly syndrome, Hurler and Huler/Scheie  
CC syndromes.  
XX  
SQ Sequence 592 AA;  
Query Match 100.0%; Score 131; DB 22; Length 592;  
Best Local Similarity 50.0%; Pred. No. 0.0007;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;  
QY 1 XXCEXCEXXXKEXXKXXDNNKXEXXKEXXDXKXKXX 38  
DB 3 VYCEVCEFLVKEVTKLIDNNKTEKELDAFDKMKSLP 40  
RESULT 10  
AAB67289  
ID AAB67289 standard; Peptide; 25 AA.  
XX  
AC AAB67289;  
XX  
DT 20-APR-2001 (first entry)  
XX  
DE Human saposin C.  
XX  
KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.  
XX  
OS Homo sapiens.  
XX  
PN EP1072609-A2.  
XX  
PD 31-JAN-2001.  
XX  
PF 30-JUN-2000; 2000EP-0305504.  
XX  
PR 30-JUN-1999; 99JP-0185155.  
XX  
PA (SAKA/) SAKANAKA M.  
PA (TANA/) TANAKA J.  
PA (SATO/) SATO K.  
XX  
PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;  
XX  
DR WPI; 2001-204263/21.  
XX  
PT Use of prosaposin-related peptides or derivatives as cytoprotective  
PT agents, for suppressing apoptosis or apoptosis-like cell death -  
XX  
PS Disclosure; Page 12; 41pp; English.  
XX  
CC The present invention relates to use of a prosaposin-related peptide  
CC or derivative, in the production of a medicament for use in  
CC preventing or delaying cell death, or in promoting the expression  
CC of cell death supporting gene product Bcl-XL. The invention is  
CC useful for preventing the death of cells e.g. brain cells,  
CC neurons and cardiac muscle cells, in vitro or ex vivo.  
XX  
SQ Sequence 25 AA;  
Query Match 64.9%; Score 85; DB 22; Length 25;  
Best Local Similarity 52.0%; Pred. No. 0.2;  
Matches 13; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXKXXDNNKXEXXKEXXDX 30  
DB 1 CEFLVKEVTKLIDNNKTEKELDAF 25  
RESULT 11  
AAR70773  
ID AAR70773 standard; peptide; 22 AA.  
XX  
AC AAR70773;  
XX  
DT 30-AUG-1995 (first entry)  
XX  
DE Saposin-C neurotrophic peptide.  
XX  
KW Saposin-C; neuron; myelination; nervous system; neuroblastoma;  
KW neurotrophic peptide; multiple sclerosis; leukoencephalitis;  
KW adrenal leukodystrophy.  
XX  
OS Homo sapiens.  
XX  
PN WO9503821-A.  
XX  
PD 09-FEB-1995.  
XX  
PF 28-JUL-1994; 94WO-US08453.  
XX  
PR 30-JUL-1993; 93US-0100247.  
PR 21-APR-1994; 94US-0232513.  
XX  
PA (OBRI/) OBRIEN J S.  
XX  
PI Kishimoto Y, Obrien JS;  
XX  
DR WPI; 1995-082029/11.  
XX  
PT Stimulating neural cell out-growth and myelination - with  
PT pro:saposin, saposin C or new neurotrophic peptide(s) from  
PT cytokine(s), for treating nervous system diseases  
XX  
PS Disclosure; Page 30; 50pp; English.  
XX  
CC The peptide given in AAR70773, corresponding to amino acids 8-29 of  
CC human saposin-C (AAR70784), promotes neurite outgrowth in vitro.  
CC A consensus sequence was determined by comparing the peptide with  
CC hematopoietic and neuropoietic cytokines, and neurotrophic peptides  
CC (AAR70774-82) were identified in the AB loop of human ciliary  
CC neurotrophic factor, interleukins-6, -2, -3 and -gamma,  
CC erythropoietin and leukocyte inhibitory factor, and in helix C of  
CC human interleukin-1-beta and oncostatin-M. Prosaponin (AAR70783)  
CC and saposin-C also promoted nerve cell myelination ex vivo.  
XX  
SQ Sequence 22 AA;  
Query Match 58.8%; Score 77; DB 16; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXXKXXDNNKXEXXKEXX 27  
DB 1 CEFLVKEVTKLIDNNKTEKEL 22  
RESULT 12  
AAW30013  
ID AAW30013 standard; peptide; 22 AA.  
XX  
AC AAW30013;  
XX  
DT 14-APR-1998 (first entry)  
XX  
DE Prosaposin-derived peptide 22-mer.



XX Human; prosaposin; neural disorder; demyelination disorder;  
KW neural cell death; inhibition; myelination; neurite outgrowth;  
KW neuropathic pain; peripheral nerve disorder; neuroma; mononeuropathy;  
KW polyneuropathy; dorsal root ganglia; spinal cord; brainstem; thalamus..  
XX Homo sapiens.  
OS WO9732895-A1.  
PN  
XX  
XX 12-SEP-1997.  
PD  
XX  
PF 05-MAR-1997; 97WO-US04143.  
XX  
XX 05-MAR-1996; 96US-0611307.  
PR  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI O'Brien JS;  
XX  
DR WPI; 1997-470538/43.  
XX  
XX Prosaposin-derived peptide - useful for therapy of neural or  
PT demyelination disorders in neural tissue  
PF  
XX  
PS Claim 9; Page 52; 69pp; English.  
XX  
CC The present sequence represents a prosaposin-derived peptide. A method  
CC has been developed of alleviating or preventing neuropathic pain in a  
CC subject, comprising administering an effective amount of an active  
CC fragment of prosaposin to the subject. The prosaposin-derived peptide  
CC is useful for therapy of neural or demyelination disorders in neural  
CC tissue. It can be used to stimulate neurite outgrowth, inhibit neural  
CC cell death, promote myelination or inhibit demyelination. The method  
CC is used to alleviate neuropathic pain resulting from a peripheral nerve  
CC disorder, such as neuroma, nerve compression, crush or stretch and  
CC incomplete nerve transection, mononeuropathy or polyneuropathy.  
CC Alternatively the neuropathic pain results from a disorder of the  
CC dorsal root ganglia, spinal cord, brainstem, thalamus or cortex.  
XX  
SQ Sequence 22 AA;  
Query Match 58.8%; Score 77; DB 18; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXKXXDNNKXEXX 27  
DB 1 CEFLVKEVTKLIDNNKTEKIL 22  
RESULT 13  
AAW66127  
ID AAW66127 standard; peptide; 22 AA.  
XX  
AC AAW66127;  
XX  
DT 17-NOV-1998 (first entry)  
XX  
DE Prosaposin receptor agonist #1.  
XX  
KW prosaposin; receptor agonist; neuropathic pain; neurite outgrowth;  
KW neural cell death; nerve disorder; side effect.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9839357-A1.  
XX  
PD 11-SEP-1998.  
XX  
PF 11-SEP-1997; 97WO-US16062.  
XX

PR 05-MAR-1997; 97WO-US04143.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI O'Brien JS;  
XX  
DR WPI; 1998-495790/42.  
DR N-PSDB; AAV07664.  
XX  
PT Use of prosaposin receptor agonists - for alleviating neuropathic  
PT pain, inhibiting sensory or motor neuropathy, or inhibiting neural  
PT cell death  
XX  
PS Claim 3; Page 2; 67pp; English.  
XX  
CC The invention relates to prosaposin receptor agonists. Also claimed  
CC are: (1) methods for alleviating neuropathic pain or inhibiting the  
CC onset of neuropathic pain, comprising administering a prosaposin receptor  
CC agonist; (2) inhibiting sensory or motor neuropathy, comprising  
CC contacting neuronal cells with a composition comprising a prosaposin  
CC receptor agonist; (3) methods for stimulating neurite outgrowth,  
CC inhibiting neural cell death, promoting myelination, or inhibiting  
CC demyelination comprising contacting neuronal cells with a composition  
CC comprising a prosaposin receptor agonist which has 14-50 amino acids and  
CC comprises the sequence of a prosaposin derived protein. The processes  
CC may be used for treatment of neuropathic pain resulting from peripheral  
CC nerve disorders (e.g. neuroma, nerve compression, nerve crush, nerve  
CC stretch, incomplete nerve transection, mononeuropathy or polyneuropathy)  
CC or disorders of dorsal root ganglia, the spinal cord, the brainstem, the  
CC thalamus or the cortex. The receptor agonists do not cause undesirable  
CC side effects. The present sequence represents a specifically claimed  
CC prosaposin receptor agonist.  
XX  
SQ Sequence 22 AA;  
Query Match 58.8%; Score 77; DB 19; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CEXXXKEXKXXDNNKXEXX 27  
DB 1 CEFLVKEVTKLIDNNKTEKIL 22  
RESULT 14  
AAW85656  
ID AAW85656 standard; Peptide; 22 AA.  
XX  
AC AAW85656;  
XX  
DT 19-JUL-1999 (first entry)  
XX  
DE Prosaposin receptor agonist.  
XX  
KW Prosaposin; saposin; prosaptides; prosaposin receptor agonists;  
KW PRA; peripheral nervous system; central nervous system; PNS; CNS;  
KW Akt; Bcl-2; therapy; treatment; apoptosis; caspase;  
KW tumour necrosis factor; TNF; cytokine; interferon gamma; IFN;  
KW inflammation; rheumatoid arthritis; Crohn's disease;  
KW irritable bowel syndrome; asthma; cardiac infarction;  
KW congestive heart failure; multiple sclerosis;  
KW acute disseminated inflammatory leukoencephalitis;  
KW progressive multifocal leukoencephalitis; Alzheimer's disease;  
KW Parkinson's disease; amyotrophic lateral sclerosis;  
KW Huntington's disease; ischemic heart disease; Guillain-Barre disease;  
KW alopecia; AIDS dementia; cerebral malaria; HTLV; neuropathy;  
KW inflammatory neurodegenerative disease; toxin-induced liver disease.  
XX  
OS Homo sapiens.  
XX  
PN WO9912559-A1.  
XX  
PD 18-MAR-1999.

XX 09-SEP-1998; 98WO-US19216.  
XX 04-JUN-1998; 98US-0088129.  
PR 09-SEP-1997; 97US-0058352.  
XX (REGC ) UNIV CALIFORNIA.  
PA O'brien JS;  
XX WPI; 1999-229139/19.  
PI Use of prosaposin receptor agonist  
XX Claim 7; Page 66; 90pp; English.

CC Prosaposin is a 70kDa glycoprotein which is proteolytically processed  
CC to generate saposins A, B, C and D, all of which are similar to each  
CC other and have a similar placement of six cysteines, a glycosylation  
CC site and conserved proline residues. Prosaposin, saposin C and  
CC prosaposin derived peptides (prosaptides), have therapeutic  
CC applications in promoting recovery after toxic, traumatic, myocardial  
CC ishchaemic, degenerative and inherited lesions to the peripheral and  
CC central nervous system. Prosaposin receptor agonists (PRAs)  
CC inhibit proinflammatory cytokine-induced apoptosis by activation of  
CC the Ser/Thr protein kinase Akt. Akt dissociates complexes of Bcl-2  
CC family members, such as BAD-Bcl-2, releasing Bcl-2 and its family  
CC members which inhibit caspases, thereby inhibiting apoptosis. An  
CC additional mechanism whereby PRAs inhibit apoptosis is by blocking  
CC activation of JNK, a proapoptotic signaling component. Within  
CC several minutes after binding to the receptor, PRAs block JNK  
CC activation induced by tumor necrosis factor-alpha (TNF alpha). The  
CC activation of JNK by TNF alpha is another well known mechanism for  
CC TNF alpha-induced, as well as other proinflammatory cytokine-induced  
CC apoptosis. The method can be used for inhibiting apoptosis which is  
CC caspase-mediated or induced by a proinflammatory cytokine, for  
CC example TNF alpha or interferon-gamma. It can be used for inhibiting  
CC apoptosis associated with a disorder such as e.g. rheumatoid  
CC arthritis, Crohn's disease, irritable bowel syndrome, asthma, cardiac  
CC infarction, congestive heart failure, multiple sclerosis, acute  
CC disseminated inflammatory leukoencephalitis, progressive multifocal  
CC leukoencephalitis, Alzheimer's disease, Huntington's disease,  
CC amyotrophic lateral sclerosis, Parkinson's disease, ischemic heart  
CC disease, Guillain-Barre disease, traumatic brain injury, traumatic  
CC spinal cord injury, alopecia, AIDS dementia, cerebral malaria, HTLV,  
CC neuropathy, inflammatory neurodegenerative disease, and toxin-induced  
CC liver disease. This peptide corresponds to amino acids 8 to 29 of  
CC human saposin C (See AAW85653) and acts as a prosaposin receptor  
CC agonist.

XX SQ Sequence 22 AA;

Query Match 58.8%; Score 77; DB 20; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 6 CEXXXKEXKXXDNNKXKEXX 27  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

RESULT 15  
AAB67305  
ID AAB67305 standard; Peptide; 22 AA.

XX AC AAB67305;

XX DT 20-APR-2001 (first entry)

XX DE Peptide #5.

XX KW Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.

OS Homo sapiens.  
XX EP1072609-A2.  
PN 31-JAN-2001.  
XX 30-JUN-2000; 2000EP-0305504.  
PF 30-JUN-1999; 99JP-0185155.  
XX (SAKA/) SAKANAKA M.  
PA (TANA/) TANAKA J.  
PA (SATO/) SATO K.

PI Sakanaka M, Tanaka J, Sato K, Morita F, Sadamoto Y;  
XX WPI; 2001-204263/21.

PT Use of prosaposin-related peptides or derivatives as cytoprotective  
PT agents, for suppressing apoptosis or apoptosis-like cell death -  
XX Disclosure; Page 28; 41pp; English.

XX The present invention relates to use of a prosaposin-related peptide  
CC or derivative, in the production of a medicament for use in  
CC preventing or delaying cell death, or in promoting the expression  
CC of cell death supporting gene product Bcl-XL. The invention is  
CC useful for preventing the death of cells e.g. brain cells,  
CC neurons and cardiac muscle cells, in vitro or ex vivo.

XX SQ Sequence 22 AA;

Query Match 58.8%; Score 77; DB 22; Length 22;  
Best Local Similarity 54.5%; Pred. No. 0.95;  
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 6 CEXXXKEXKXXDNNKXKEXX 27  
Db 1 CEFLVKEVTKLIDNNKTEKIL 22

Search completed: June 2, 2003, 14:19:05  
Job time : 35 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:17:59 ; Search time 16 Seconds  
(without alignments)  
228.319 Million cell updates/sec

Title: us-09-780-438c-6  
Perfect score: 131  
Sequence: 1 XXCEXCEXXXKXKXKXNDNNKXKXKXDXDXKXKXKX 38

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 131   | 100.0       | 527    | 1 SAHUP  | saposin precursor  |
| 2          | 114   | 87.0        | 80     | 2 S21770 | saposin-C - bovine |
| 3          | 89    | 67.9        | 81     | 2 A32026 | glucosylceramide b |
| 4          | 74    | 56.5        | 419    | 2 T18450 | hypothetical prote |
| 5          | 73    | 55.7        | 314    | 2 T15674 | hypothetical prote |
| 6          | 73    | 55.7        | 554    | 1 A28716 | saposin precursor  |
| 7          | 71    | 54.2        | 965    | 2 T00207 | P109 protein - sil |
| 8          | 70    | 53.4        | 557    | 1 JH0604 | saposin precursor  |
| 9          | 70    | 53.4        | 572    | 2 T20764 | hypothetical prote |
| 10         | 69    | 52.7        | 570    | 2 T08778 | hypothetical prote |
| 11         | 68    | 51.9        | 483    | 2 S41853 | centromere/microtu |
| 12         | 68    | 51.9        | 2285   | 2 T12796 | probable transglyc |
| 13         | 67.5  | 51.5        | 473    | 2 F70031 | cell wall-binding  |
| 14         | 67    | 51.1        | 301    | 2 T33068 | hypothetical prote |
| 15         | 67    | 51.1        | 427    | 2 A35659 | krueppel-related p |
| 16         | 67    | 51.1        | 428    | 2 S47096 | cynarase (EC 3.4.2 |
| 17         | 67    | 51.1        | 474    | 2 T12049 | cyprosin (EC 3.4.2 |
| 18         | 67    | 51.1        | 2664   | 2 T28626 | variant-specific s |
| 19         | 66.5  | 50.8        | 1377   | 2 T19214 | UDP-glucose-glycop |
| 20         | 66.5  | 50.8        | 1390   | 2 S51364 | sperm tail-specifi |
| 21         | 66    | 50.4        | 210    | 2 T28771 | hypothetical prote |
| 22         | 66    | 50.4        | 211    | 2 T25911 | hypothetical prote |
| 23         | 66    | 50.4        | 774    | 2 JC2299 | cell surface glyco |
| 24         | 66    | 50.4        | 1036   | 2 T05687 | beta-galactosidase |
| 25         | 66    | 50.4        | 1324   | 2 T01508 | mismatch repair en |
| 26         | 65.5  | 50.0        | 176    | 2 T00498 | probable AP2 domai |
| 27         | 65.5  | 50.0        | 913    | 2 T46339 | hypothetical prote |
| 28         | 65.5  | 50.0        | 1216   | 2 A28822 | 1-phosphatidylinos |
| 29         | 65.5  | 50.0        | 1216   | 2 A28821 | 1-phosphatidylinos |

|    |      |      |      |          |                    |
|----|------|------|------|----------|--------------------|
| 30 | 65   | 49.6 | 217  | 2 S23244 | hypothetical prote |
| 31 | 65   | 49.6 | 321  | 1 BWMSV4 | Mov-34 protein - m |
| 32 | 65   | 49.6 | 488  | 2 S47072 | finger protein HzF |
| 33 | 65   | 49.6 | 504  | 2 S48550 | hypothetical prote |
| 34 | 65   | 49.6 | 588  | 2 E89751 | protein C33E10.5 l |
| 35 | 65   | 49.6 | 743  | 2 A29232 | 101K malaria antig |
| 36 | 65   | 49.6 | 3228 | 2 T21381 | hypothetical prote |
| 37 | 64.5 | 49.2 | 143  | 2 S41017 | hypothetical prote |
| 38 | 64.5 | 49.2 | 165  | 2 T52114 | probable transcrip |
| 39 | 64.5 | 49.2 | 366  | 2 JQ0513 | phenylalanine dehy |
| 40 | 64.5 | 49.2 | 445  | 2 E86440 | probable chloropla |
| 41 | 64.5 | 49.2 | 2013 | 2 C71610 | probable membrane  |
| 42 | 64   | 48.9 | 126  | 2 A56657 | PfEMP2/MESA protei |
| 43 | 64   | 48.9 | 213  | 2 T46069 | hypothetical prote |
| 44 | 64   | 48.9 | 217  | 2 S43193 | KSI protein - Hydr |
| 45 | 64   | 48.9 | 219  | 2 T19897 | hypothetical prote |

ALIGNMENTS

RESULT 1

SAHUP  
saposin precursor [validated] - human  
N:Alternate names: cerebroside sulfate activator protein; co-beta-glucosidase; compon  
ein (SAP); sphingolipid activator protein A2; sulfatide sulfatase activator protein  
N:Contains: prosaposin; saposin A; saposin B; saposin C; saposin D  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1992 #sequence\_revision 17-Nov-1995 #text\_change 08-Dec-2000  
C:Accession: JX0061; A57368; A42003; C42003; D42003; A30367; S34740; S36140;  
0226; I37265; I37264  
R:Nakano, T.; Sandhoff, K.; Stuenkel, J.; Christomanou, H.; Suzuki, K.  
J. Biochem. 105, 152-154, 1989  
A:Title: Structure of full-length cDNA coding for sulfatide activator, a Co-beta-gluc  
A:Reference number: JX0061; MUID:89255151; PMID:2498298  
A:Accession: JX0061  
A:Molecule type: mRNA  
A:Residues: 1-527 <NAK>  
A:Cross-references: GB:D00422; NID:g220063; PIDN:BAA00321.1; PID:g220064  
A:Note: alternative splice form 1  
A:Accession: A57368  
A:Molecule type: mRNA  
A:Residues: 1-259,263-527 <NA2>  
A:Cross-references: GB:J03015; GB:J03086; NID:g337755; PIDN:AAB59494.1; PID:g337756  
A:Note: alternative splice form 2  
R:Rorman, E.G.; Scheinker, V.; Grabowski, G.A.  
Genomics 13, 312-318, 1992  
A:Title: Structure and evolution of the human prosaposin chromosomal gene.  
A:Reference number: A42003; MUID:92307663; PMID:1612590  
A:Accession: A42003  
A:Molecule type: DNA  
A:Residues: 50-140 <ROR>  
A:Cross-references: GB:M86181  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107236)  
A:Accession: B42003  
A:Molecule type: DNA  
A:Residues: 185-259;263-276 <RO2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107237)  
A:Accession: C42003  
A:Molecule type: DNA  
A:Residues: 305-393 <RO3>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107238); sequence  
A:Accession: D42003  
A:Molecule type: DNA  
A:Residues: 399-487 <RO4>  
A:Note: sequence extracted from NCBI backbone (NCBIN:107235, NCBIP:107239); sequence  
R:Rorman, E.G.; Grabowski, G.A.  
Genomics 5, 486-492, 1989  
A:Title: Molecular cloning of a human co-beta-glucosidase cDNA: evidence that four sp  
A:Reference number: A30367; MUID:90129043; PMID:2515150  
A:Accession: A30367  
A:Molecule type: mRNA  
A:Residues: 1-259,263-527 <RO5>

A;Cross-references: GB:J03077; NID:gl83230; PIDN:AAA52560.1; PID:gl83231  
A;Note: alternative splice form 2  
R;Hiraiwa, M.; O'Brien, J.S.; Kishimoto, Y.; Galdzicka, M.; Fluharty, A.L.; Ginns, E.I.; Arch. Biochem. Biophys. 304, 110-116, 1993  
A;Title: Isolation, characterization, and proteolysis of human prosaposin, the precursor  
A;Reference number: S34740; MUID:93311991; PMID:8323276  
A;Accession: S34740  
A;Molecule type: protein  
A;Residues: 17-24;165-172;180-189;301-305 <HIR>  
R;Tynnelae, J.; Palmer, D.N.; Baumann, M.; Haltia, M. FEBS Lett. 330, 8-12, 1993  
A;Title: Storage of saposins A and D in infantile neuronal ceroid-lipofuscinosis.  
A;Reference number: S36140; MUID:93380576; PMID:8370464  
A;Accession: S36140  
A;Molecule type: protein  
A;Residues: 'XX',62,'X',64-65,'X',67-79,'X',81-84 <TTY>  
A;Note: saposin A  
A;Accession: S36141  
A;Molecule type: protein  
A;Residues: 'XXX',413-414,'X',416-428,'X',430-434 <TY2>  
A;Note: saposin D  
R;Holtzschmidt, H.; Sandhoff, K.; Kwon, H.Y.; Harzer, K.; Nakano, T.; Suzuki, K. J. Biol. Chem. 266, 7556-7560, 1991  
A;Title: Sulfatide activator protein. Alternative splicing that generates three mRNAs and  
A;Reference number: S36988; MUID:91210267; PMID:2019586  
A;Accession: S36988  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-259,263-527 <HO1>  
A;Cross-references: EMBL:M60255; NID:g337759; PIDN:AAA36594.1; PID:g337760  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-9; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-259,263-527 <HO2>  
A;Cross-references: EMBL:M60257; NID:g337764; PIDN:AAA36595.1; PID:g337765  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-0; corresponds to alternative splicing  
A;Accession: S36990  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-240,'S',242-259,261-527 <HO3>  
A;Cross-references: EMBL:M60258; NID:g337766; PIDN:AAA36596.1; PID:g337767  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991  
A;Note: cerebroside sulfate activator protein mutant MU-6; corresponds to alternative splicing  
R;Kondoh, K.; Hinenno, T.; Sano, A.; Kakimoto, Y. Biochem. Biophys. Res. Commun. 181, 286-292, 1991  
A;Title: Isolation and characterization of prosaposin from human milk.  
A;Reference number: PS0330; MUID:92068206; PMID:1958198  
A;Accession: PS0330  
A;Molecule type: protein  
A;Residues: 17-24,'X',26 <KON>  
A;Experimental source: milk  
R;Kretz, K.A.; Carson, G.S.; Morimoto, S.; Kishimoto, Y.; Fluharty, A.L.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 87, 2541-2544, 1990  
A;Title: Characterization of a mutation in a family with saposin B deficiency: a glycosylation  
A;Reference number: A35985; MUID:90207231; PMID:2320574  
A;Accession: A35985  
A;Molecule type: mRNA  
A;Residues: 213-221 <KRE>  
A;Cross-references: GB:M32221  
A;Accession: B35985  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-259,263-527 <KR2>  
A;Cross-references: GB:M32221; NID:g337761; PIDN:AAA60303.1; PID:g337762  
A;Experimental source: lymphoblast  
A;Accession: C35985  
A;Molecule type: mRNA  
A;Residues: 213-216,'I',218-221 <KR3>  
A;Note: sequence from patients with activator-deficient metachromatic leukodystrophy; the  
R;Fuerst, W.; Schubert, J.; Machleidt, W.; Meyer, H.E.; Sandhoff, K.

Eur. J. Biochem. 192, 709-714, 1990  
A;Title: The complete amino-acid sequences of human ganglioside GM2 activator protein  
A;Reference number: S13195; MUID:91006165; PMID:2209618  
A;Accession: S13196  
A;Molecule type: protein  
A;Residues: 195-259,263-277 <FUE>  
R;Morimoto, S.; Martin, B.M.; Yamamoto, Y.; Kretz, K.A.; O'Brien, J.S.; Kishimoto, Y. Proc. Natl. Acad. Sci. U.S.A. 86, 3389-3393, 1989  
A;Title: Saposin A: second cerebroside activator protein.  
A;Reference number: A32784; MUID:89240739; PMID:2717620  
A;Accession: A32784  
A;Molecule type: protein  
A;Residues: 60-84;86-107;109-119;125-134 <MOR>  
R;O'Brien, J.S.; Kretz, K.A.; Dewji, N.; Wenger, D.A.; Esch, F.; Fluharty, A.L. Science 241, 1098-1101, 1988  
A;Title: Coding of two sphingolipid activator proteins (SAP-1 and SAP-2) by same gene  
A;Reference number: A41240; MUID:88321660; PMID:2842863  
A;Accession: A41240  
A;Molecule type: mRNA  
A;Residues: 'GSSR',18-259,263-299,'D',301-302,'D',304-527 <OAB>  
A;Cross-references: GB:J03086  
R;Dewji, N.N.; Wenger, D.A.; O'Brien, J.S. Proc. Natl. Acad. Sci. U.S.A. 84, 8652-8656, 1987  
A;Title: Nucleotide sequence of cloned cDNA for human sphingolipid activator protein  
A;Reference number: S02289; MUID:88068647; PMID:2825202  
A;Accession: S02289  
A;Status: significant sequence differences  
A;Molecule type: mRNA  
A;Cross-references: EMBL:J03015  
A;Note: this sequence corrected by A41240  
A;Note: part of this sequence, including the amino end of the mature protein, was determined  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 369, 1361-1365, 1988  
A;Title: Complete amino-acid sequence of the naturally occurring A(2) activator protein  
A;Reference number: S02028; MUID:89207118; PMID:3242555  
A;Accession: S02028  
A;Molecule type: protein  
A;Residues: 195-259,263-276 <KLE>  
R;Fuerst, W.; Machleidt, W.; Sandhoff, K. Biol. Chem. Hoppe-Seyler 369, 317-328, 1988  
A;Title: The precursor of sulfatide activator protein is processed to three different  
A;Reference number: S00813; MUID:89000190; PMID:3048308  
A;Accession: S00813  
A;Molecule type: protein  
A;Residues: 410-487 <FU2>  
R;Kleinschmidt, T.; Christomanou, H.; Braunitzer, G. Biol. Chem. Hoppe-Seyler 368, 1571-1578, 1987  
A;Title: Complete amino-acid sequence and carbohydrate content of the naturally occurring  
A;Reference number: S00226; MUID:88163077; PMID:3442600  
A;Accession: S00226  
A;Molecule type: protein  
A;Residues: 314-393 <KL2>  
R;Vaccaro, A.M.; Salvioli, R.; Barca, A.; Tatti, M.; Ciaffoni, F.; Maras, B.; Sicilia J. Biol. Chem. 270, 9953-9960, 1995  
A;Title: Structural analysis of saposin C and B. Complete localization of disulfide bonds  
A;Reference number: A57297; MUID:95247790; PMID:7730378  
A;Contents: annotation; disulfide bonds; glycosylation  
R;Holtzschmidt, H.; Sandhoff, K.; Fuerst, W.; Kwon, H.Y.; Schnabel, D.; Suzuki, K. FEBS Lett. 280, 267-270, 1991  
A;Title: The organization of the gene for the human cerebroside sulfate activator protein  
A;Reference number: I37264; MUID:91192146; PMID:2013321  
A;Accession: I37265  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 59-125 <RES>  
A;Cross-references: EMBL:X57107; NID:g30234; PIDN:CAA40391.1; PID:g30235  
A;Accession: I37264  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 307-516 <RE2>  
A;Cross-references: EMBL:X57108; NID:g30232; PIDN:CAA40392.1; PID:g1565257  
A;Note: sequence revised relative to PID:g30233 (corrected coding region)  
C;Genetics:











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Job time : 17 secs



RL Proc. Natl. Acad. Sci. U.S.A. 84:8652-8656(1987).  
RN [6]  
RP PARTIAL SEQUENCE OF 60-142.  
RX MEDLINE-89240739; PubMed=2717620;  
RA Morimoto S., Martin B.M., Yamamoto Y., Kretz K.A., O'Brien J.S.,  
RA Kishimoto Y.;  
RT "Saposin A: second cerebroside activator protein.";  
RN Proc. Natl. Acad. Sci. U.S.A. 86:3389-3393(1989).  
RP [7]  
RX SEQUENCE OF 195-263 FROM N.A.  
RA MEDLINE-86130593; PubMed=2868718;  
RA Dewji N.N., Wenger D.A., Fujibayashi S., Donoviel M., Esch F.,  
RA Hill F., O'Brien J.S.;  
RT "Molecular cloning of the sphingolipid activator protein-1 (SAP-1),  
RT the sulfatide sulfatase activator.";  
RL Biochem. Biophys. Res. Commun. 134:989-994(1986).  
RN [8]  
RP SEQUENCE OF 195-274.  
RC TISSUE-Kidney;  
RX MEDLINE-91006165; PubMed=2209618;  
RA Furst W., Schubert J., Machleidt W., Meyer H.E., Sandhoff K.;  
RT "The complete amino-acid sequences of human ganglioside GM2 activator  
RT protein and cerebroside sulfate activator protein.";  
RL Eur. J. Biochem. 192:709-714(1990).  
RN [9]  
RP SEQUENCE OF 195-274.  
RX MEDLINE-89207118; PubMed=3242555;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence of the naturally occurring A2 activator  
RT protein for enzymic sphingomyelin degradation: identity to the  
RT sulfatide activator protein (SAP-1).";  
RL Biol. Chem. Hoppe-Seyler 369:1361-1365(1988).  
RN [10]  
RP SEQUENCE OF 311-390.  
RX MEDLINE-88163077; PubMed=3442600;  
RA Kleinschmidt T., Christomanou H., Braunitzer G.;  
RT "Complete amino-acid sequence and carbohydrate content of the  
RT naturally occurring glucosylceramide activator protein (A1 activator)  
RT absent from a new human Gaucher disease variant.";  
RL Biol. Chem. Hoppe-Seyler 368:1571-1578(1987).  
RN [11]  
RP SEQUENCE OF 407-484.  
RX MEDLINE-89000190; PubMed=3048308;  
RA Furst W., Machleidt W., Sandhoff K.;  
RT "The precursor of sulfatide activator protein is processed to three  
RT different proteins.";  
RL Biol. Chem. Hoppe-Seyler 369:317-328(1988).  
RN [12]  
RP PARTIAL SEQUENCE OF 405-484.  
RX MEDLINE-89025876; PubMed=2845979;  
RA Morimoto S., Martin B.M., Kishimoto Y., O'Brien J.S.;  
RT "Saposin D: a sphingomyelinase activator.";  
RL Biochem. Biophys. Res. Commun. 156:403-410(1988).  
RN [13]  
RP SEQUENCE OF 17-26.  
RC TISSUE-Milk;  
RX MEDLINE-92068206; PubMed=1958198;  
RA Kondoh K., Hineno T., Sano A., Kakimoto Y.;  
RT "Isolation and characterization of prosaposin from human milk.";  
RL Biochem. Biophys. Res. Commun. 181:286-292(1991).  
RN [14]  
RP PARTIAL SEQUENCE (SAPOSIN B), AND STRUCTURE OF CARBOHYDRATES.  
RC TISSUE-Urine;  
RX MEDLINE-20032116; PubMed=10562467;  
RA Fluharty A.L., Lombardo C., Louis A., Stevens R.L., Whitelegge J.,  
RA Waring A.J., To T., Fluharty C.B., Faull K.F.;  
RT "Preparation of the cerebroside sulfate activator (CSAct or saposin B)  
RT from human urine.";  
RL Mol. Genet. Metab. 68:391-403(1999).  
RN [15]  
RP STRUCTURE OF CARBOHYDRATE ON ASN-215.  
RX MEDLINE-21110404; PubMed=11180632;  
RA Faull K.F., Johnson J., Kim M.J., To T., Whitelegge J.P.,

RA Stevens R.L., Fluharty C.B., Fluharty A.L.;  
RT "Structure of the asparagine-linked sugar chains of porcine kidney and  
RT human urine cerebroside sulfate activator protein.";  
RL J. Mass Spectrom. 35:1416-1424(2000).  
RN [16]  
RP MASS SPECTROMETRY.  
RC TISSUE-Urine;  
RX MEDLINE-99441404; PubMed=10510427;  
RA Faull K.F., Whitelegge J.P., Higginson J., To T., Johnson J.,  
RA Krutchinsky A.N., Standing K.G., Waring A.J., Stevens R.L.,  
RA Fluharty C.B., Fluharty A.L.;  
RT "Cerebroside sulfate activator protein (Saposin B): chromatographic  
RT and electrospray mass spectrometric properties.";  
RL J. Mass Spectrom. 34:1040-1054(1999).  
RN [17]  
RP VARIANT MLD ILE-217.  
RX MEDLINE-90147748; PubMed=2302219;  
RA Rafi M.A., Zhang X.-L., Degala G., Wenger D.A.;  
RT "Detection of a point mutation in sphingolipid activator protein-1  
RT mRNA in patients with a variant form of metachromatic  
RT leukodystrophy.";  
RL Biochem. Biophys. Res. Commun. 166:1017-1023(1990).  
RN [18]  
RP SEQUENCE FROM N.A., AND VARIANT MLD ILE-217.  
RX MEDLINE-90207231; PubMed=2320574;  
RA Kretz K.A., Carson G.S., Morimoto S., Kishimoto Y., Fluharty A.L.,  
RA O'Brien J.S.;  
RT "Characterization of a mutation in a family with saposin B  
RT deficiency: a glycosylation site defect.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2541-2544(1990).  
RN [19]  
RP VARIANT MLD SER-241, SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE-91210267; PubMed=2019586;  
RA Holtschmidt H., Sandhoff K., Kwon H.Y., Harzer K., Nakano T.,  
RA Suzuki K.;  
RT "Sulfatide activator protein. Alternative splicing that generates  
RT three mRNAs and a newly found mutation responsible for a clinical  
RT disease.";  
RL J. Biol. Chem. 266:7556-7560(1991).  
RN [20]  
RP VARIANT GAUCHER PHE-388.  
RX MEDLINE-91285107; PubMed=2060627;  
RA Schnabel D., Schroeder M., Sandhoff K.;  
RT "Mutation in the sphingolipid activator protein 2 in a patient with a  
RT variant of Gaucher disease.";  
RL FEBS Lett. 284:57-59(1991).  
RN [21]  
RP REVIEW ON MLD VARIANTS.  
RX MEDLINE-95170731; PubMed=7866401;  
RA Gieselmann V., Zlotogora J., Harris A., Wenger D.A., Morris C.P.;  
RT "Molecular genetics of metachromatic leukodystrophy.";  
RL Hum. Mutat. 4:233-242(1994).  
CC -!- FUNCTION: The lysosomal degradation of sphingolipids takes place  
CC by the sequential action of specific hydrolases. Some of these  
CC enzymes require specific low-molecular mass, non-enzymic proteins:  
CC the sphingolipids activator proteins (coproteins).  
CC -!- FUNCTION: Saposin A and saposin C stimulate the hydrolysis of  
CC glucosylceramide by beta-glucosylceramidase (EC 3.2.1.45) and  
CC galactosylceramide by beta-galactosylceramidase (EC 3.2.1.46).  
CC Saposin C apparently acts by combining with the enzyme and acidic  
CC lipid to form an activated complex, rather than by solubilizing  
CC the substrate.  
CC -!- FUNCTION: Saposin B stimulates the hydrolysis of galacto-  
CC cerebroside sulfate by arylsulfatase A (EC 3.1.6.8), GM1  
CC gangliosides by beta-galactosidase (EC 3.2.1.23) and  
CC globotriaosylceramide by alpha-galactosidase A (EC 3.2.1.22).  
CC Saposin B forms a solubilizing complex with the substrates of the  
CC sphingolipid hydrolases.  
CC -!- FUNCTION: Saposin D is a specific sphingomyelin phosphodiesterase  
CC activator (EC 3.1.4.12).  
CC -!- SUBUNIT: Saposin B is a homodimer.  
CC -!- SUBCELLULAR LOCATION: Lysosomal.  
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; sap-mu-0 (shown here),







## RESULT 5

```
SAP_RAT STANDARD; PRT; 554 AA.
AC P10960; Q62841; Q64190;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
GN PSAP OR SGPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC TISSUE=Sertoli cells;
RX MEDLINE=89000647; PubMed=3048385;
RA Collard M.W., Sylvester S.R., Tsuruta J.K., Griswold M.D.;
RT "Biosynthesis and molecular cloning of sulfated glycoprotein 1
RT secreted by rat Sertoli cells: sequence similarity with the
RT 70-kilodalton precursor to sulfatide/GM1 activator.";
RL Biochemistry 27:4557-4564(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=96128541; PubMed=8573994;
RA Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
RT "Molecular role of sulfated glycoprotein-1 (SGP-1/prosaposin) in
RT Sertoli cells.";
RL Histol. Histopathol. 10:1023-1034(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testicle;
RX MEDLINE=96175245; PubMed=8601692;
RA Morales C.R., El-Alfy M., Zhao Q., Igdoura S.A.;
RT "Expression and tissue distribution of rat sulfated glycoprotein-1
RT (prosaposin).";
RL J. Histochem. Cytochem. 44:327-337(1996).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; M19936; AAA42136.1; -
DR EMBL; S81353; AAB36042.2; -
DR EMBL; S81373; AAB36233.2; -
DR PIR; A28716; A28716.
DR InterPro; IPR003119; Sapa.
DR InterPro; IPR000004; SapB.
DR Pfam; PF02199; SAPA; 2.
DR ProDom; PD001732; SapB; 4.
DR SMART; SM00162; SAPA; 2.
DR SMART; SM00118; SAPB; 4.
KW Sulfation; Signal; Glycoprotein; Repeat.
FT SIGNAL 1 16
FT CHAIN 17 554 SULFATED GLYCOPROTEIN 1.
FT DOMAIN 21 54 SAPOSIN-LIKE TYPE A 1.
FT DOMAIN 61 138 SAPOSIN-LIKE TYPE B 1.
FT DOMAIN 193 274 SAPOSIN-LIKE TYPE B 2.
FT DOMAIN 310 391 SAPOSIN-LIKE TYPE B 3.
FT DOMAIN 435 516 SAPOSIN-LIKE TYPE B 4.
FT DOMAIN 521 554 SAPOSIN-LIKE TYPE A 2.
FT DISULFID 63 138 BY SIMILARITY.
FT DISULFID 66 132 BY SIMILARITY.
FT DISULFID 94 106 BY SIMILARITY.
FT DISULFID 197 270 BY SIMILARITY.
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FT DISULFID 200 264 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 314 387 BY SIMILARITY.
FT DISULFID 317 381 BY SIMILARITY.
FT DISULFID 345 356 BY SIMILARITY.
FT DISULFID 439 512 BY SIMILARITY.
FT DISULFID 442 506 BY SIMILARITY.
FT DISULFID 470 481 BY SIMILARITY.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 115 115 P -> L (IN REF. 2 AND 3).
FT CONFLICT 299 299 D -> E (IN REF. 2).
FT CONFLICT 462 462 I -> V (IN REF. 3).
FT CONFLICT 527 527 W -> R (IN REF. 3).
FT CONFLICT 536 536 S -> M (IN REF. 3).
SQ SEQUENCE 554 AA; 61123 MW; DFE3F3A3A0520C6B CRC64;
Query Match 55.7%; Score 73; DB 1; Length 554;
Best Local Similarity 22.9%; Pred. No. 40;
Matches 8; Conservative 22; Mismatches 5; Indels 0; Gaps
QY 1 XXCEXCEXXXKEXXKXXDNNKXKEXXDXDXKXCX 35
Db 61 LPCDICKTVVTEAGNLLKDNATEEELHYLEKTC 95
RESULT 6
SAP_MOUSE STANDARD; PRT; 557 AA.
AC Q61207; Q64219; Q64006; Q60861;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfated glycoprotein 1 precursor (SGP-1) (Prosaposin).
GN PSAP OR SGPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92272718; PubMed=1590788;
RA Tsuda M., Sakiyama T., Endo H., Kitagawa T.;
RT "The primary structure of mouse saaposin.";
RL Biochem. Biophys. Res. Commun. 184:1266-1272(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94272317; PubMed=8003952;
RA Sprecher-Levy H., Orr-Urtreger A., Lonai P., Horowitz M.;
RT "Murine prosaposin: expression in the reproductive system of a gene
RT implicated in human genetic disease.";
RL Cell. Mol. Biol. 40:233-233(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96084310; PubMed=8565332;
RA Cao Q.P., Crain W.R.;
RT "Expression of SGP-1 mRNA in preimplantation mouse embryos.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Zhao Q.Q., Hay N.N., Morales C.R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- SIMILARITY: CONTAINS 2 SAPOSIN A-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 4 SAPOSIN B-TYPE DOMAINS.
CC -----
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RA Johnson A.F., Dedhia N., Martienssen R., McComble W.R.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-cv. Columbia;  
 RX MEDLINE-99444907; PubMed-10517319;  
 RA Ade J., Belzile F., Philippe H., Doutriaux M.P.;  
 RT "Four mismatch repair paralogs coexist in Arabidopsis thaliana:  
 RL AtMSH2, AtMSH3, AtMSH6-1 and AtMSH6-2";  
 RN Mol. Gen. Genet. 262:239-249(1999).  
 RP [3]  
 RC SEQUENCE FROM N.A.  
 RL STRAIN-cv. Columbia;  
 RX MEDLINE-20083488; PubMed-10617198;  
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
 RL Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,  
 RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Mueller M.,  
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Schmidheini T.,  
 RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidheini T.,  
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
 RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,  
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,  
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
 RA Weitzenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,  
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,  
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
 RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,  
 RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,  
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,  
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,  
 RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,  
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,  
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fartmann B., Grandrath K., Dauner D., Herzl A.,  
 RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,  
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
 RA Chedfor F., Cooke R., Berger C., Monfort A., Casacuberta E.,  
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,  
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,  
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,  
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,  
 RA Nelson J., Spiehl J., Ryan E., Andrews S., Geisel C., Layman D.,  
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
 RA Chen E., Marra M., Martienssen R., McComble W.R.;  
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
 RL thaliana";  
 RL Nature 402:769-777(1999).  
 CC -1- FUNCTION: INVOLVED IN POST-REPLICATIVE DNA-MISMATCH REPAIR (BY  
 CC SIMILARITY).  
 CC -1- SUBUNIT: HETERODIMER OF MSH2 AND MSH6 (GTBP) (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.  
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DR EMBL; AF001535; AAB57798.1; -;  
 DR EMBL; AJ245967; CAB53337.1; -;  
 DR EMBL; AF001308; AAC78699.1; -;  
 DR EMBL; AL161493; CAB80700.1; -;  
 DR InterPro; IPR000432; Muts\_C;  
 DR InterPro; IPR002863; Muts\_N;  
 DR InterPro; IPR002999; Tudor;  
 DR Pfam; PF00488; Muts\_C; 1;  
 DR Pfam; PF01624; Muts\_N; 2;  
 DR ProDom; PD001263; Muts\_C; 1;  
 DR SMART; SM00534; Muts\_C; 1;  
 DR SMART; SM00533; Muts\_C; 1;  
 DR SMART; SM00333; Tudor; 1;  
 DR PROSITE; PS00486; DNA\_MISMATCH\_REPAIR\_2; 1;  
 KW DNA repair; ATP-binding; DNA-binding.  
 FT NP\_BIND 1083 1090 ATP (POTENTIAL).  
 FT CONFLICT 316 318 ADP -> GPKSLLL (IN REF. 1).  
 FT CONFLICT 383 383 Q -> QVRRAGNL (IN REF. 1).  
 FT CONFLICT 852 852 P -> PGIINLHILILANCTASHIISLP (IN  
 FT REF. 1).  
 SQ SEQUENCE 1324 AA; 146797 MW; 787A340272CF979C CRC64;  
 Query Match 50.4%; Score 66; DB 1; Length 1324;  
 Best Local Similarity 22.9%; Pred. No. 3.9e+02;  
 Matches 8; Conservative 22; Mismatches 5; Indels 0; Gaps 0;  
 QY 4 EXCEXXXKEXXNDNNKXEXXDXDXKXKXKX 38  
 DB 233 EVCESEDDVELVDENEMDEEELVEKDEETSKVN 267  
 RESULT 13  
 PIB1\_BOVIN STANDARD; PRT; 1216 AA.  
 ID PIB1\_BOVIN  
 AC P10894;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JUL-1989 (Rel. 11, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1  
 DE (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC-154).  
 GN PLCB1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-88270496; PubMed-2455601;  
 RA Katan M., Kriz R.W., Totty N., Philp R., Meldrum E., Aldape R.A.,  
 RA Knopf J.L., Parker P.J.;  
 RT "Determination of the primary structure of PLC-154 demonstrates  
 RT diversity of phosphoinositide-specific phospholipase C activities.";  
 RL Cell 54:171-177(1988).  
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES  
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS  
 CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE  
 CC C ENZYMES.  
 CC -1- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-  
 CC bisphosphate + H(2)O -> D-myo-inositol 1,4,5-trisphosphate +  
 CC diacylglycerol.  
 CC -1- COFACTOR: Calcium.  
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS  
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.  
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS  
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.  
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.  
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Search completed: June 2, 2003, 14:19:23  
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:17:24 ; Search time 29 seconds  
(without alignments)  
269.993 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXCEXXXKEXXXXXNNKXEXKEXXXXXKXXCXXX 38

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 78    | 59.5        | 1334   | 5     | 097322 plasmodium  |
| 2          | 74    | 56.5        | 520    | 13    | Q8UVZ4 brachydanio |
| 3          | 74    | 56.5        | 522    | 13    | Q9DG82 brachydanio |
| 4          | 74    | 56.5        | 594    | 5     | 077337 plasmodium  |
| 5          | 73    | 55.7        | 238    | 5     | Q18276 caenorhabdi |
| 6          | 73    | 55.7        | 294    | 5     | Q95X03 naegleria f |
| 7          | 73    | 55.7        | 307    | 5     | Q9BKM2 naegleria f |
| 8          | 71.5  | 54.6        | 540    | 16    | Q8XHG9 clostridium |
| 9          | 71    | 54.2        | 86     | 10    | Q8WLM2 solanum cha |
| 10         | 71    | 54.2        | 257    | 3     | Q01803 pneumocysti |
| 11         | 71    | 54.2        | 744    | 5     | Q9VD23 drosophila  |
| 12         | 71    | 54.2        | 965    | 5     | Q15997 bombyx mori |
| 13         | 70    | 53.4        | 231    | 2     | Q93EJ8 francisella |
| 14         | 70    | 53.4        | 257    | 5     | Q9N5S7 caenorhabdi |
| 15         | 70    | 53.4        | 441    | 5     | Q9U9P3 drosophila  |
| 16         | 70    | 53.4        | 953    | 5     | Q9Y125 drosophila  |

|    |      |      |      |    |        |                    |
|----|------|------|------|----|--------|--------------------|
| 17 | 69.5 | 53.1 | 285  | 13 | Q9DGH7 | Q9dgh7 gallus gall |
| 18 | 69.5 | 53.1 | 312  | 13 | Q9DGH8 | Q9dgh8 gallus gall |
| 19 | 69   | 52.7 | 397  | 4  | Q9BT47 | Q9bt47 homo sapien |
| 20 | 69   | 52.7 | 444  | 4  | O60405 | O60405 homo sapien |
| 21 | 69   | 52.7 | 496  | 4  | O75760 | O75760 homo sapien |
| 22 | 69   | 52.7 | 567  | 4  | Q9H6Z4 | Q9h6z4 homo sapien |
| 23 | 69   | 52.7 | 570  | 4  | Q9UG74 | Q9ug74 homo sapien |
| 24 | 69   | 52.7 | 1065 | 3  | Q01828 | Q01828 pneumocysti |
| 25 | 68.5 | 52.3 | 1092 | 3  | Q9UVY2 | Q9uvy2 pneumocysti |
| 26 | 68   | 51.9 | 359  | 5  | 097326 | 097326 plasmodium  |
| 27 | 68   | 51.9 | 1000 | 3  | Q96VI9 | Q96vi9 pneumocysti |
| 28 | 68   | 51.9 | 2285 | 9  | O64046 | O64046 bacterioph  |
| 29 | 68   | 51.9 | 2285 | 16 | O31976 | O31976 bacillus su |
| 30 | 67   | 51.1 | 204  | 5  | Q9N5Z8 | Q9n5z8 caenorhabdi |
| 31 | 67   | 51.1 | 301  | 5  | O61765 | O61765 caenorhabdi |
| 32 | 67   | 51.1 | 304  | 5  | Q8WT00 | Q8wt00 plasmodium  |
| 33 | 67   | 51.1 | 427  | 4  | Q02313 | Q02313 homo sapien |
| 34 | 67   | 51.1 | 568  | 4  | Q8TD23 | Q8td23 homo sapien |
| 35 | 67   | 51.1 | 1618 | 11 | Q9QX19 | Q9qx19 rattus norv |
| 36 | 67   | 51.1 | 2081 | 10 | Q9LH98 | Q9lh98 arabidopsis |
| 37 | 67   | 51.1 | 2664 | 5  | Q26033 | Q26033 plasmodium  |
| 38 | 66.5 | 50.8 | 516  | 5  | Q9Y155 | Q9y155 drosophila  |
| 39 | 66.5 | 50.8 | 540  | 5  | Q9W0X8 | Q9w0x8 drosophila  |
| 40 | 66.5 | 50.8 | 1377 | 5  | P91854 | P91854 caenorhabdi |
| 41 | 66   | 50.4 | 185  | 5  | Q9Y0V9 | Q9y0v9 drosophila  |
| 42 | 66   | 50.4 | 185  | 5  | Q8SYA0 | Q8sya0 drosophila  |
| 43 | 66   | 50.4 | 210  | 5  | O02124 | O02124 caenorhabdi |
| 44 | 66   | 50.4 | 211  | 5  | P91488 | P91488 caenorhabdi |
| 45 | 66   | 50.4 | 296  | 5  | Q95UP8 | Q95up8 dictyosteli |

ALIGNMENTS

RESULT 1

|        |                                                                        |              |      |      |     |  |
|--------|------------------------------------------------------------------------|--------------|------|------|-----|--|
| O97322 |                                                                        |              |      |      |     |  |
| ID     | O97322                                                                 | PRELIMINARY; | PRT; | 1334 | AA. |  |
| AC     | O97322;                                                                |              |      |      |     |  |
| DT     | 01-MAY-1999 (TREMBLrel. 10, Created)                                   |              |      |      |     |  |
| DT     | 01-OCT-2000 (TREMBLrel. 15, Last sequence update)                      |              |      |      |     |  |
| DT     | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                    |              |      |      |     |  |
| DE     | Hypothetical 160.8 kDa protein.                                        |              |      |      |     |  |
| GN     | PFC1010W, MAL3P7.32.                                                   |              |      |      |     |  |
| OS     | Plasmodium falciparum (isolate 3D7).                                   |              |      |      |     |  |
| OC     | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.           |              |      |      |     |  |
| OX     | NCBI_TaxID=36329;                                                      |              |      |      |     |  |
| RN     | [1]                                                                    |              |      |      |     |  |
| RP     | SEQUENCE FROM N.A.                                                     |              |      |      |     |  |
| RC     | STRAIN=3D7;                                                            |              |      |      |     |  |
| RX     | MEDLINE=99376085; PubMed=10448855;                                     |              |      |      |     |  |
| RA     | Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,           |              |      |      |     |  |
| RA     | Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,          |              |      |      |     |  |
| RA     | Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T., |              |      |      |     |  |
| RA     | Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,       |              |      |      |     |  |
| RA     | Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,        |              |      |      |     |  |
| RA     | Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,           |              |      |      |     |  |
| RA     | Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;                 |              |      |      |     |  |
| RT     | "The complete nucleotide sequence of chromosome 3 of Plasmodium        |              |      |      |     |  |
| RT     | falciparum ."                                                          |              |      |      |     |  |
| RL     | Nature 400:532-538(1999).                                              |              |      |      |     |  |
| DR     | EMBL; AL034559; CAB39073.2; -                                          |              |      |      |     |  |
| KW     | Hypothetical protein.                                                  |              |      |      |     |  |
| SW     | SEQUENCE 1334 AA; 160847 MW; E3577E84C7E0C8E5 CRC64;                   |              |      |      |     |  |

Query Match

Best Local Similarity 59.5%; Score 78; DB 5; Length 1334;

Matches 10; Conservative 23; Mismatches 5; Indels 0; Gaps 0;

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Db 881 RKLQNLDMKEKWKYENNNNNKDKNKNKCNKIL 918



Query Match 55.7%; Score 73; DB 5; Length 307;







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2003, 14:18:29 ; Search time 15 Seconds  
(without alignments)  
74.538 Million cell updates/sec

Title: US-09-780-438C-6  
Perfect score: 131  
Sequence: 1 XXCEXCEXXXKEXXXKXXDNNKXEXXDXDXKXXCXXKXX 38

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 131   | 100.0       | 80     | 1     | US-08-100-247-3   |
| 2          | 131   | 100.0       | 80     | 1     | US-08-483-146A-3  |
| 3          | 131   | 100.0       | 80     | 1     | US-08-232-513A-4  |
| 4          | 131   | 100.0       | 80     | 1     | US-08-484-594A-3  |
| 5          | 131   | 100.0       | 523    | 1     | US-08-100-247-2   |
| 6          | 131   | 100.0       | 523    | 1     | US-08-483-146A-2  |
| 7          | 131   | 100.0       | 523    | 1     | US-08-232-513A-3  |
| 8          | 131   | 100.0       | 523    | 1     | US-08-484-594A-2  |
| 9          | 77    | 58.8        | 22     | 1     | US-08-100-247-1   |
| 10         | 77    | 58.8        | 22     | 1     | US-08-483-146A-1  |
| 11         | 77    | 58.8        | 22     | 1     | US-08-232-513A-1  |
| 12         | 77    | 58.8        | 22     | 1     | US-08-484-594A-1  |
| 13         | 77    | 58.8        | 22     | 4     | US-09-231-159-1   |
| 14         | 77    | 58.8        | 22     | 4     | US-08-611-307-1   |
| 15         | 77    | 58.8        | 22     | 4     | US-09-148-030-1   |
| 16         | 72    | 55.0        | 22     | 4     | US-09-231-159-8   |
| 17         | 72    | 55.0        | 22     | 4     | US-08-611-307-8   |
| 18         | 70    | 53.4        | 22     | 1     | US-08-483-146A-9  |
| 19         | 70    | 53.4        | 22     | 1     | US-08-232-513A-18 |
| 20         | 70    | 53.4        | 22     | 1     | US-08-484-594A-9  |
| 21         | 70    | 53.4        | 22     | 4     | US-09-231-159-7   |
| 22         | 70    | 53.4        | 22     | 4     | US-08-611-307-7   |
| 23         | 68    | 51.9        | 2285   | 4     | US-09-308-375-2   |
| 24         | 64.5  | 49.2        | 143    | 4     | US-09-180-100-10  |
| 25         | 64.5  | 49.2        | 159    | 4     | US-09-180-100-23  |
| 26         | 64.5  | 49.2        | 360    | 4     | US-09-180-100-11  |
| 27         | 64.5  | 49.2        | 376    | 4     | US-09-180-100-22  |

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| 28 | 63.5 | 48.5 | 314 | 1 | US-08-444-231-19  | Sequence 19, Appl |
| 29 | 63.5 | 48.5 | 314 | 1 | US-08-152-443A-19 | Sequence 19, Appl |
| 30 | 63.5 | 48.5 | 314 | 5 | PCT-US95-17083-4  | Sequence 4, Appl  |
| 31 | 62   | 47.3 | 514 | 4 | US-08-796-899-25  | Sequence 25, Appl |
| 32 | 62   | 47.3 | 708 | 4 | US-08-235-836C-76 | Sequence 76, Appl |
| 33 | 61   | 46.6 | 18  | 1 | US-08-100-247-5   | Sequence 5, Appl  |
| 34 | 61   | 46.6 | 18  | 1 | US-08-483-146A-5  | Sequence 5, Appl  |
| 35 | 61   | 46.6 | 18  | 1 | US-08-232-513A-6  | Sequence 6, Appl  |
| 36 | 61   | 46.6 | 18  | 1 | US-08-484-594A-5  | Sequence 5, Appl  |
| 37 | 61   | 46.6 | 18  | 4 | US-09-231-159-20  | Sequence 20, Appl |
| 38 | 61   | 46.6 | 18  | 4 | US-08-611-307-20  | Sequence 20, Appl |
| 39 | 61   | 46.6 | 18  | 4 | US-09-148-030-2   | Sequence 2, Appl  |
| 40 | 61   | 46.6 | 445 | 4 | US-08-845-258-38  | Sequence 38, Appl |
| 41 | 61   | 46.6 | 445 | 4 | US-08-990-571-38  | Sequence 38, Appl |
| 42 | 61   | 46.6 | 445 | 4 | US-08-723-142A-38 | Sequence 38, Appl |
| 43 | 61   | 46.6 | 445 | 4 | US-09-528-784A-38 | Sequence 38, Appl |
| 44 | 61   | 46.6 | 666 | 4 | US-09-528-784A-85 | Sequence 85, Appl |
| 45 | 61   | 46.6 | 727 | 2 | US-08-475-844-9   | Sequence 9, Appl  |

ALIGNMENTS

RESULT 1  
US-08-100-247-3  
; Sequence 3, Application US/08100247  
; Patent No. 5571787  
; GENERAL INFORMATION:  
; APPLICANT: O'BRIEN, JOHN S.  
; APPLICANT: KISHIMOTO, YASUO  
; TITLE OF INVENTION: PROSAPOSIN AS A NEUTROTROPHIC FACTOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
; CITY: NEWPORT BEACH  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/100,247  
; FILING DATE: 19930730  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: OBRIEN.002A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; IMMEDIATE SOURCE:  
; CLONE: SAPOSIN C  
US-08-100-247-3

Query Match 100.0%; Score 131; DB 1; Length 80;  
Best Local Similarity 50.0%; Pred. No. 1.6e-05;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;



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| Qy | 1 | XXCXCXXXXXXKXXDNNKXEKEXDXXDKYCKXX           | 38 |
|    |   | : : : : : : : : : : : : : : : : : : : : : : |    |
| Db | 3 | VYCEVCEFLVKEVTKLIDNNKTEKEILDADFCKMCKLP      | 40 |

## RESULT 2

US-08-146A-3  
; Sequence 3, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson and Bear  
; STREET: 620 Newport Center Blvd. 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,146A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-235-8550  
; TELEFAX: 619-235-0176  
; TELEX:

### RESULT 3

US-08-232-513A-4  
; Sequence 4, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides  
; TITLE OF INVENTION: as Therapeutic Agents  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP

```

; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; FEATURE:
;
; NAME/KEY: Peptide
; LOCATION: 1..80
; OTHER INFORMATION: /label- Saposin_C
;
; US-08-232-513A-4

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## RESULTS AND DISCUSSION

US-08-484-594A-3  
Sequence 3, Application US/08484594A  
Patent No. 5714459  
GENERAL INFORMATION:  
APPLICANT: O'Brien, John S.  
APPLICANT: Kishimoto, Yasuo  
TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPIC PEPTIDES  
TITLE OF INVENTION: DERIVED THEREFROM  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive, Sixteenth Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,594A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/100,247

FILING DATE: 30-JUL-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Israelsen, Ned A  
 REGISTRATION NUMBER: 29,655  
 REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-235-8550  
 TELEFAX: 619-235-0176  
 TELEX:

Query Match 100.0%; Score 131; DB 1; Length 80;  
Best Local Similarity 50.0%; Pred. NO. 1.6e-05;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 5  
 US-08-100-247-2  
 ; Sequence 2, Application US/08100247  
 ; Patent No. 5571787  
 ; GENERAL INFORMATION:  
 ; APPLICANT: O'BRIEN, JOHN S.  
 ; APPLICANT: KISHIMOTO, YASUO  
 ; TITLE OF INVENTION: PROSAPOSIN AS A NEUROTROPIC FACTOR  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
 ; STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
 ; CITY: NEWPORT BEACH  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 92660  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0; Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/100,247  
 ; FILING DATE: 19930730  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israelsen, Ned A.  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: OBRIEN.002A  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 523 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: N-terminal  
 ; IMMEDIATE SOURCE:  
 ; CLONE: PROSAPOSIN  
 ; US-08-100-247-2

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Query Match 100.0%; Score 131; DB 1; Length 523;
Best Local Similarity 50.0%; Pred. No. 0.00018;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
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**Db**           **312 VYCEVCFVKVETKLIDNNKTEKEILDAFDMCSKLP 349**

RESULT 6  
US-08-483-146A-2  
; Sequence 2, Application US/08483146A  
; Patent No. 5696080  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; APPLICANT: Kishimoto, Yasuo  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPIC PEPTIDES DERIVED  
; TITLE OF INVENTION: THEREFROM  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:

Query Match 100.0%; Score 131; DB 1; Length 523;  
Best Local Similarity 50.0%; Pred. NO. 0.00018;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7  
US-08-232-513A-3  
; Sequence 3, Application US/08232513A  
; Patent No. 5700909  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.

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; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..523
; OTHER INFORMATION: /label= Hum_prosaposin
; US-08-232-513A-3

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Query Match 100.0%; Score 131; DB 1; Length 523;
Best Local Similarity 50.0%; Pred. No. 0.00018;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
US-08-484-594A-2
; Sequence 2, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/484,594A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,247  
 ; FILING DATE: 30-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Israelsen, Ned A  
 ; REGISTRATION NUMBER: 29,655  
 ; REFERENCE/DOCKET NUMBER: MYELOS.002DV2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 619-235-8550  
 ; TELEFAX: 619-235-0176  
 ; TELEX:  
 ;  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 523 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: N-terminal  
 ;  
 ; US-08-484-594A-2

Query Match 100.0%; Score 131; DB 1; Length 523;  
Best Local Similarity 50.0%; Pred. No. 0.00018;  
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCXXXXXXKXXXDNKKEXDXDKCXKXX 38  
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Db 312 VYCEVCELVKEVTKLIDNNKTEKEILDADKMCSKLP 349

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1
2
3
4
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6
7
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; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; IMMEDIATE SOURCE:
; CLONE: 22-MER FRAGMENT
US-08-100-247-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXEXX 27
Db 1 CEFLVKEVTKLIDNKNKEIL 22

RESULT 10
US-08-483-146A-1
; Sequence 1, Application US/08483146A
; Patent No. 5696080
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: COMPRISING PROSAPOSIN AND NEUROTROPHIC PEPTIDES DERIVED
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Blvd. 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,146A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: MYELOS.002DV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-483-146A-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXEXX 27
Db 1 CEFLVKEVTKLIDNKNKEIL 22

RESULT 11

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US-08-232-513A-1
; Sequence 1, Application US/08232513A
; Patent No. 5700909
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; TITLE OF INVENTION: Prosaposin and Cytokine-Derived Peptides
; TITLE OF INVENTION: as Therapeutic Agents
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,513A
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,247
; FILING DATE: 30-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..22
; OTHER INFORMATION: /label= SapC
US-08-232-513A-1
Query Match 58.8%; Score 77; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 0.3;
Matches 12; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 6 CEXXXKEXXXDNNKXEXX 27
Db 1 CEFLVKEVTKLIDNKNKEIL 22

RESULT 12
US-08-484-594A-1
; Sequence 1, Application US/08484594A
; Patent No. 5714459
; GENERAL INFORMATION:
; APPLICANT: O'Brien, John S.
; APPLICANT: Kishimoto, Yasuo
; TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:

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; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-438A-1

Query Match 100.0%; Score 131; DB 9; Length 40;
Best Local Similarity 50.0%; Pred. No. 3.2e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCXXXXXKXNDNNKXKEXXDXDXKXCXKXX 38
 3 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 40
Db

RESULT 3
US-09-767-007A-3
; Sequence 3, Application US/09767007A
; Patent No. US20020077275A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial peptide
US-09-767-007A-3

Query Match 100.0%; Score 131; DB 10; Length 80;
Best Local Similarity 50.0%; Pred. No. 7.7e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCXXXXXKXNDNNKXKEXXDXDXKXCXKXX 38
 3 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 40
Db

RESULT 4
US-09-753-126-3
; Sequence 3, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-000600US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
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; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-753-126-3

Query Match 100.0%; Score 131; DB 10; Length 80;
Best Local Similarity 50.0%; Pred. No. 7.7e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCXXXXXKXNDNNKXKEXXDXDXKXCXKXX 38
 3 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 40
Db

RESULT 5
US-10-043-487-340
; Sequence 340, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Shigella Flexneri
US-10-043-487-340

Query Match 100.0%; Score 131; DB 9; Length 209;
Best Local Similarity 50.0%; Pred. No. 0.00026;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCEXCXXXXXKXNDNNKXKEXXDXDXKXCXKXX 38
 3 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 200
Db

RESULT 6
US-09-767-007A-2
; Sequence 2, Application US/09767007A
; Patent No. US20020077275A1
; GENERAL INFORMATION:
; APPLICANT: John S. O'Brien
; APPLICANT: Yasuo Kishimoto
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: SAPOSIN C AND NEUROTROPHIC PEPTIDES DERIVED THEREFROM
; FILE REFERENCE: MYELOS.2DC1C1
; CURRENT APPLICATION NUMBER: US/09/767,007A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 08/958,970
; PRIOR FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 523
; TYPE: PRT
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; ORGANISM: homo sapiens
US-09-767-007A-2

Query Match 100.0%; Score 131; DB 10; Length 523;
Best Local Similarity 50.0%; Pred. No. 0.00082;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECXXXXXKXXXXXNDNNKXKEXXDXDXKXCKXX 38
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Db 312 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 349

RESULT 7
US-09-870-759-60
; Sequence 60, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-60

Query Match 100.0%; Score 131; DB 9; Length 524;
Best Local Similarity 50.0%; Pred. No. 0.00082;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECXXXXXKXXXXXNDNNKXKEXXDXDXKXCKXX 38
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Db 313 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 350

RESULT 8
US-09-870-759-61
; Sequence 61, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-61

Query Match 100.0%; Score 131; DB 9; Length 527;
Best Local Similarity 50.0%; Pred. No. 0.00083;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECXXXXXKXXXXXNDNNKXKEXXDXDXKXCKXX 38
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Db 316 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 353

RESULT 9
US-10-060-036-73
; Sequence 73, Application US/100600036
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; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-73

Query Match 100.0%; Score 131; DB 9; Length 527;
Best Local Similarity 50.0%; Pred. No. 0.00083;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 1 XXCECXXXXXKXXXXXNDNNKXKEXXDXDXKXCKXX 38
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Db 316 VYCEVCEFLVKEVTKLIDNNKTEKEILDADFDMCSKLP 353

RESULT 10
US-09-753-126-4
; Sequence 4, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000US
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
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; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric
; OTHER INFORMATION: SapC-linker-GCB polypeptide
US-09-753-126-4

Query Match 100.0%; Score 131; DB 10; Length 592;
Best Local Similarity 50.0%; Pred. No. 0.00096;
Matches 19; Conservative 19; Mismatches 0; Indels 0; Gaps 0;
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Search completed: June 2, 2003, 14:21:06  
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